78224   192007   MY

From:	Seharaseyon, Jegatheesan
Sent:	Monday, June 05, 2006 10:49 AM
To:	STIC-Biotech/ChemLib
Subject:	10/063534

Please search SEQ ID NO: 30 in the pending and allowed databases.
Also please search with a word size of 6 amino acids.

Thanks

J.Seharaseyon
Art Unit 1647
Remsen 4C61
Mailbox 4C70
Phone: (571)-272-0892
Fax: (571)-273-0892

****
Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:_____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____

****
Type of Search
NA#_____ AA#:_____
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other (Specify):_____

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OM protein - protein search, using sw model

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                    GenCore version 5.1.9
            Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Run on: June 6, 2006, 21:26:54 ; Search time 16 Seconds
                               (without alignments)
                               52.766 Million cell updates/sec

Title: US-10-063-534-30
Perfect score: 73
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Scoring table: 1
Scoring table: OLIGO
Searched: Gapop 60.0 , Gapext 60.0
Word size :   58871 seqs, 11565156 residues
Word size :   6

Total number of hits satisfying chosen parameters: 246

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Published_Applications_AA_New:*
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         4: /EMC_Celerra_SID53/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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         6: /EMC_Celerra_SID53/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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         8: /EMC_Celerra_SID53/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 73 | 100.0 | 73 | 7 | US-11-101-316-30 | Sequence 30, Appl |
| 2 | 9 | 12.3 | 294 | 6 | US-10-953-349-25258 | Sequence 25258, A |
| 3 | 9 | 12.3 | 314 | 6 | US-10-953-349-25257 | Sequence 25257, A |
| 4 | 9 | 12.3 | 515 | 6 | US-10-953-349-21352 | Sequence 21352, A |
| 5 | 9 | 12.3 | 516 | 6 | US-10-953-349-21351 | Sequence 21351, A |
| 6 | 9 | 12.3 | 521 | 6 | US-10-953-349-21350 | Sequence 21350, A |
| 7 | 8 | 11.0 | 16 | 7 | US-11-257-581-13 | Sequence 13, Appl |
| 8 | 8 | 11.0 | 173 | 7 | US-11-293-697-3431 | Sequence 3431, Appl |
| 9 | 8 | 11.0 | 206 | 6 | US-10-511-937-2938 | Sequence 2938, Ap |
| 10 | 8 | 11.0 | 208 | 6 | US-10-953-349-15677 | Sequence 15677, A |
| 11 | 8 | 11.0 | 232 | 6 | US-10-514-462-7 | Sequence 7, Appl |
| 11 | 8 | 11.0 | 234 | 7 | US-10-196-749-482 | Sequence 482, App |
| 12 | 8 | 11.0 | 243 | 7 | US-11-320-192-9 | Sequence 9, Appli |
| 13 | 8 | 11.0 | 243 | 7 | US-11-320-192-12 | Sequence 12, Appl |
| 14 | 8 | 11.0 | 314 | 6 | US-10-953-349-34590 | Sequence 34590, A |
| 15 | 8 | 11.0 | 338 | 7 | US-11-101-450-95 | Sequence 95, Appl |
| 16 | 8 | 11.0 | 378 | 7 | US-10-953-349-34588 | Sequence 34588, A |
| 17 | 8 | 11.0 | 397 | 7 | US-11-244-452-7 | Sequence 7, Appli |
| 18 | 8 | 11.0 | 418 | 6 | US-10-953-349-32813 | Sequence 32813, A |
| 19 | 8 | 11.0 | 467 | 6 | US-10-953-349-16 | Sequence 16, Appl |
| 20 | 8 | 11.0 | 480 | 7 | US-10-196-749-16 | Sequence 16, Appl |
| 21 | 8 | 11.0 | 487 | 6 | US-11-301-554-336 | Sequence 336, App |
| 22 | 8 | 11.0 | 508 | 6 | US-10-196-749-230 | Sequence 230, App |
| 23 | 8 | 11.0 | 521 | 6 | US-10-953-349-32268 | Sequence 32268, A |
| 24 | 8 | 11.0 | 531 | 7 | US-10-953-349-32267 | Sequence 32267, A |
| 25 | 8 | 11.0 | 531 | 7 | US-11-257-581-4 | Sequence 4, Appli |
| 26 | 8 | 11.0 | 531 | 7 | US-11-257-581-5 | Sequence 5, Appli |
| 27 | 8 | 11.0 | 531 | 7 | US-11-257-581-6 | Sequence 6, Appli |
| 28 | 8 | 11.0 | 538 | 7 | US-11-140-450-37 | Sequence 37, Appl |
| 29 | 8 | 11.0 | 544 | 7 | US-11-257-581-1 | Sequence 1, Appli |
| 30 | 8 | 11.0 | 544 | 7 | US-11-257-581-2 | Sequence 2, Appli |
| 31 | 8 | 11.0 | 544 | 7 | US-11-257-581-3 | Sequence 3, Appli |
| 32 | 8 | 11.0 | 721 | 7 | US-11-293-697-3470 | Sequence 3470, Ap |
| 33 | 8 | 11.0 | 813 | 6 | US-10-196-749-466 | Sequence 466, App |
| 34 | 8 | 11.0 | 837 | 6 | US-10-196-749-454 | Sequence 454, App |
| 35 | 8 | 11.0 | 837 | 6 | US-10-540-394-1 | Sequence 1, Appli |
| 36 | 8 | 11.0 | 837 | 6 | US-10-540-394-4 | Sequence 4, Appli |
| 37 | 8 | 11.0 | 837 | 6 | US-10-540-394-7 | Sequence 7, Appli |
| 38 | 8 | 11.0 | 837 | 6 | US-10-540-394-10 | Sequence 10, Appl |
| 39 | 8 | 11.0 | 972 | 7 | US-11-255-147-8 | Sequence 8, Appli |
| 40 | 8 | 11.0 | 1015 | 6 | US-10-505-928-359 | Sequence 359, App |
| 41 | 8 | 11.0 | 4590 | 6 | US-10-505-928-569 | Sequence 569, App |
| 42 | 7 | 9.6 | 69 | 6 | US-10-953-349-36432 | Sequence 36432, A |
| 43 | 7 | 9.6 | 75 | 6 | US-10-953-349-36431 | Sequence 36431, A |
| 44 | 7 | 9.6 | 82 | 6 | US-10-953-349-28006 | Sequence 28006, A |
| 45 | 7 | 9.6 | 84 | 6 | US-10-196-749-186 | Sequence 186, App |

ALIGNMENTS

RESULT 1
US-11-101-316-30

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; Sequence 30, Application US/11101316
; Publication No. US20060099657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; TITLE OF INVENTION: UNDEREXPRESSED IN MELANOMA
; FILE REFERENCE: P2230R1C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 30
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-101-316-30
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Query Match   100.0%;   Score 73;   DB 7;   Length 73;
Best Local Similarity   100.0%;   Pred. No. 9.6e-62;
Matches   73;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy         61 AQPRGEGEKVGDG 73
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Db         61 AQPRGEGEKVGDG 73
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RESULT 2

US-10-953-349-25258
; Sequence 25258, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 25258
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (130)..(130)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (276)..(276)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (278)..(278)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-25258

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Db   11 LLLLLLLLL 19

Query Match   12.3%; Score 9; DB 6; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 3
US-10-953-349-25257
; Sequence 25257, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 25257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (150)..(150)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (296)..(296)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (298)..(298)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-25257

Query Match   12.3%; Score 9; DB 6; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 4
US-10-953-349-21352
; Sequence 21352, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 21352
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-21352

Qy   2 LLLLLLLLL 10
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Db   31 LLLLLLLLL 39

Query Match   12.3%; Score 9; DB 6; Length 515;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 5
US-10-953-349-21351
; Sequence 21351, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 21351
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-21351

Qy   4 LLLLLLLLL 12
        |||||||||
Db   17 LLLLLLLLL 25

Query Match   12.3%; Score 9; DB 6; Length 516;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 6
US-10-953-349-21350
; Sequence 21350, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30

Qy   4 LLLLLLLLL 12
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Db   18 LLLLLLLLL 26

; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
;
; SEQ ID NO 21350
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-21350

  Query Match   12.3%; Score 9; DB 6; Length 521;
  Best Local Similarity   100.0%; Pred. No. 0.21;
  Matches   9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   4 LLLLLLLL 12
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Db   23 LLLLLLLL 31

RESULT 7
US-11-257-581-13
; Sequence 13, Application US/11257581
; Publication No. US20060093614A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Gray D.
; APPLICANT: Sako, Dianne S.
; APPLICANT: Kumar, Ravindra
; APPLICANT: Sullivan, Francis
; APPLICANT: McDonagh, Tom
; TITLE OF INVENTION: Platelet Glycoprotein IB Alpha Fusion Polypeptides and
; TITLE OF INVENTION: Methods of Use Thereof
; FILE REFERENCE: 22058-503
; CURRENT APPLICATION NUMBER: US/10/068,426
; CURRENT FILING DATE: 2005-10-24
; PRIOR APPLICATION NUMBER: 2002-02-06
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/266,838
; PRIOR FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 13
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(16)
; OTHER INFORMATION: Signal Peptide
US-11-257-581-13

  Query Match   11.0%; Score 8; DB 7; Length 16;
  Best Local Similarity   100.0%; Pred. No. 0.1;
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Qy   6 LLLLLLLL 13
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Db   3 LLLLLLLL 10

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US-11-293-697-3431
; Sequence 3431, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 3431
; LENGTH: 173

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3431

  Query Match   11.0%; Score 8; DB 7; Length 173;
  Best Local Similarity   100.0%; Pred. No. 0.74;
  Matches   8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   6 LLLLLLLL 13
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Db   13 LLLLLLLL 20

RESULT 9
US-10-511-937-2938
; Sequence 2938, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50661200104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 2938
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2938

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  Matches   8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   38 LLLLLLLL 45

RESULT 10
US-10-953-349-15677
; Sequence 15677, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
;
; SEQ ID NO 15677
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-15677

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Db   84 LLLLLLL 91

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-514-462-7
Sequence 7, Application US/10514462
Publication No. US20060088909A1
GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Virus-Like Particles, Methods of Preparation, And Immunogenic
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 050508-2210
; CURRENT APPLICATION NUMBER: US/10/514,462
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: 60/381,557
; PRIOR FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
;
; SEQ ID NO 7
; LENGTH: 232
; TYPE: PRT
; ORGANISM: extracellular coding domain of the FI gene
US-10-514-462-7

Qy   6 LLLLLLL 13
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Db   14 LLLLLLL 21

Query Match   11.0%; Score 8; DB 6; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
US-10-196-749-482
Sequence 482, Application US/10196749
Publication No. US20060094864A1
GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
;
; SEQ ID NO 482
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-482

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Db   19 LLLLLLL 26

Query Match   11.0%; Score 8; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
US-11-320-192-9
Sequence 9, Application US/11320192
Publication No. US20060104973A1
GENERAL INFORMATION:
; APPLICANT: He, Zhigang
; APPLICANT: Wang, Kevin C.
; APPLICANT: Kim, Jieun A.
; TITLE OF INVENTION: Reducing NgR-p75 Mediated Inhibition of Axon
; TITLE OF INVENTION: Regeneration
; FILE REFERENCE: CMCC-1043
; CURRENT APPLICATION NUMBER: US/11/320,192
; CURRENT FILING DATE: 2005-12-27
; PRIOR APPLICATION NUMBER: US/10/211,157
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 9
; LENGTH: 243
; TYPE: PRT
; ORGANISM: mouse
US-11-320-192-9

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Db   6 LLLLLLL 13

Query Match   11.0%; Score 8; DB 7; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
US-11-320-192-12
Sequence 12, Application US/11320192
Publication No. US20060104973A1
GENERAL INFORMATION:
; APPLICANT: He, Zhigang
; APPLICANT: Wang, Kevin C.
; APPLICANT: Kim, Jieun A.
; TITLE OF INVENTION: Reducing NgR-p75 Mediated Inhibition of Axon
; TITLE OF INVENTION: Regeneration
; FILE REFERENCE: CMCC-1043
; CURRENT APPLICATION NUMBER: US/11/320,192
; CURRENT FILING DATE: 2005-12-27
; PRIOR APPLICATION NUMBER: US/10/211,157
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1

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;   FEATURE:
;     OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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;   Publication No. US20060107345A1
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;     APPLICANT: ALEXANDROV, Nickolai et al.
;     TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;     TITLE OF INVENTION: ENCODED THERBY
;     FILE REFERENCE: 2750-1579PUS2
;     CURRENT APPLICATION NUMBER: US/10/953,349
;     CURRENT FILING DATE: 2004-09-30
;     NUMBER OF SEQ ID NOS: 40252
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1171	8	11.0	234	4	US-09-833-245-1191	Sequence 1191, Ap
1172	8	11.0	234	3	US-09-833-245-1322	Sequence 1322, Ap

Search completed: June 9, 2006, 00:30:15
Job time : 199 secs

OM protein - protein search, using sw model

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on: June 6, 2006, 21:14:43 ; Search time 50 Seconds
(without alignments)
127.795 Million cell updates/sec

Title: US-10-063-534-30
Perfect score: 73
Sequence: 1 MLLLTLLLLLLLKGSCLEWW..........PAMTCSQAQPRGEGEKVGDG 73

Scoring table: OLIGO
             Gapop 60.0 , Gapext 60.0

Searched: 650591 seqs, 87530628 residues

Word size :   6

Total number of hits satisfying chosen parameters: 2840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Issued_Patents_AA:*
    1: /EMC_Celerra_SID3/ptodata/2/iaa/5_COMB.pep:*
    2: /EMC_Celerra_SID3/ptodata/2/iaa/6_COMB.pep:*
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    4: /EMC_Celerra_SID3/ptodata/2/iaa/H_COMB.pep:*
    5: /EMC_Celerra_SID3/ptodata/2/iaa/pCTUS_COMB.pep:*
    6: /EMC_Celerra_SID3/ptodata/2/iaa/RE_COMB.pep:*
    7: /EMC_Celerra_SID3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB	ID	Description
1	73	100.0	73	2	US-10-012-231A-22	Sequence 22, Appli
2	73	100.0	73	2	US-10-015-389A-22	Sequence 22, Appl
3	73	100.0	73	2	US-10-006-768A-22	Sequence 22, Appl
4	73	100.0	73	2	US-10-015-671A-22	Sequence 22, Appl
5	73	100.0	73	2	US-10-015-393A-22	Sequence 22, Appl
6	73	100.0	73	2	US-10-011-833A-22	Sequence 22, Appl
7	73	100.0	73	2	US-10-006-041A-22	Sequence 22, Appl
8	73	100.0	73	2	US-10-012-064A-22	Sequence 22, Appl
9	73	100.0	73	3	US-10-015-392A-22	Sequence 22, Appl
10	73	100.0	73	3	US-10-011-795B-22	Sequence 22, Appl
11	73	100.0	73	3	US-10-015-386A-22	Sequence 22, Appl
12	73	100.0	73	3	US-10-012-121A-22	Sequence 22, Appl
13	73	100.0	73	3	US-10-006-485A-22	Sequence 22, Appl
14	73	100.0	73	3	US-10-006-746A-22	Sequence 22, Appl
15	73	100.0	73	3	US-10-012-752A-22	Sequence 22, Appl
16	73	100.0	73	3	US-10-017-253A-22	Sequence 22, Appl
17	73	100.0	73	3	US-10-015-519A-22	Sequence 22, Appl
18	73	100.0	73	3	US-10-015-715A-22	Sequence 22, Appl
19	73	100.0	73	3	US-10-007-236A-22	Sequence 22, Appl
20	10	13.7	689	2	US-10-232-200-73	Sequence 73, Appl
21	10	13.7	689	2	US-09-232-197-73	Sequence 73, Appl
22	10	13.7	689	2	US-09-232-201-73	Sequence 73, Appl
23	10	13.7	689	2	US-09-232-195-73	Sequence 73, Appl
24	10	13.7	689	1	US-09-405-504A-73	Sequence 73, Appl
25	9	12.3	21	1	US-07-715-397A-2	Sequence 2, Appli
26	9	12.3	21	1	US-08-060-833-2	Sequence 2, Appli
27	9	12.3	21	1	US-08-419-824-2	Sequence 2, Appli
28	9	12.3	21	1	US-08-848-580-2	Sequence 2, Appli
29	9	12.3	21	2	US-08-488-123-2	Sequence 2, Appli
30	9	12.3	21	5	PCT-U092-04537-8	Sequence 8, Appli
31	9	12.3	26	2	US-09-336-536-59	Sequence 59, Appl
32	9	12.3	98	2	US-09-336-999C-4280	Sequence 4280, Ap
33	9	12.3	101	2	US-09-513-999C-4281	Sequence 4281, Ap
34	9	12.3	104	2	US-09-248-796A-27204	Sequence 27204, A
35	9	12.3	120	2	US-09-270-767-58991	Sequence 58991, A
36	9	12.3	131	2	US-08-938-548B-2	Sequence 2, Appli
37	9	12.3	131	2	US-08-939-093A-2	Sequence 2, Appli
38	9	12.3	131	2	US-09-211-823C-2	Sequence 2, Appli
39	9	12.3	131	2	US-09-737-379A-2	Sequence 2, Appli
40	9	12.3	213	2	US-09-336-536-58	Sequence 58, Appl
41	9	12.3	239	2	US-09-767-43613	Sequence 43613, A
42	9	12.3	500	1	US-07-755-573C-8	Sequence 8, Appli
43	9	12.3	500	2	US-09-519-878-2	Sequence 2, Appli
44	9	12.3	520	2	US-09-949-016-10586	Sequence 10586, A
45	9	12.3	546	2	US-09-746-359A-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-10-012-231A-22

Sequence 22, Application US/10012231A
Patent No. 6924355
GENERAL INFORMATION:
;   APPLICANT: Baker, Kevin P.
;   APPLICANT: Botstein, David
;   APPLICANT: Desnoyers, Luc
;   APPLICANT: Eaton, Dan I.
;   APPLICANT: Ferrara, Napoleone
;   APPLICANT: Fong, Sherman
;   APPLICANT: Gao, Wei-Qiang
;   APPLICANT: Goddard, Audrey
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Grimaldi, Christopher J.
;   APPLICANT: Gurney, Austin L.
;   APPLICANT: Hillan, Kenneth J.
;   APPLICANT: Pan, James
;   APPLICANT: Paoni, Nicholas F.
;   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;   TITLE OF INVENTION: Acids Encoding the Same
;   FILE REFERENCE: P2830P1C23
;   CURRENT APPLICATION NUMBER: US/10/012,231A
;   CURRENT FILING DATE: 2002-06-10
;   PRIOR Application removed - See File Wrapper or Palm
;   NUMBER OF SEQ ID NOS: 477
;   SEQ ID NO 22
;   LENGTH: 73
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: 1-15
;   OTHER INFORMATION: Signal peptide.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 3-18
;   OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-012-231A-22

Query Match   100.0%;   Score 73;   DB 2;   Length 73;
Best Local Similarity   100.0%;
Matches   73;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 MLLLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60

Qy   61 AQPRGEGEKVGDG 73

RESULT 2
US-10-015-389A-22
; Sequence 22, Application US/10015389A
; Patent No. 6936436
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C48
; CURRENT APPLICATION NUMBER: US/10/015,389A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-015-389A-22

Query Match   100.0%; Score 73; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.7e-65;
Matches   73; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPFPSFLCLLPHRPAMTCSQ 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPFPSFLCLLPHRPAMTCSQ 60

Qy   61 AQPRGEGEKVGDG 73
           |||||||||||||
Db   61 AQPRGEGEKVGDG 73

RESULT 3
US-10-006-768A-22
; Sequence 22, Application US/10006768A
; Patent No. 6936697
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.

RESULT 4
US-10-015-671A-22
; Sequence 22, Application US/10015671A
; Patent No. 6946263
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C47
; CURRENT APPLICATION NUMBER: US/10/015,671A
; CURRENT FILING DATE: 2001-12-11
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature

; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C10
; CURRENT APPLICATION NUMBER: US/10/006,768A
; CURRENT FILING DATE: 2002-03-05
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-006-768A-22

Query Match   100.0%; Score 73; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.7e-65;
Matches   73; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPFPSFLCLLPHRPAMTCSQ 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPFPSFLCLLPHRPAMTCSQ 60

Qy   61 AQPRGEGEKVGDG 73
           |||||||||||||
Db   61 AQPRGEGEKVGDG 73

; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-015-671A-22

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Query Match      100.0%;  Score 73;  DB 2;  Length 73;
Best Local Similarity   100.0%;  Pred. No. 2.7e-65;
Matches  73;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy  1 MLLTLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1 MLLTLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60

Qy 61 AQPRGEGEKVGDG 73
       |||||||||||||
Db 61 AQPRGEGEKVGDG 73
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RESULT 5
US-10-015-393A-22
; Sequence 22, Application US/1001539A
; GENERAL INFORMATION:
; Patent No. 6951737
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-015-393A-22

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Query Match      100.0%;  Score 73;  DB 2;  Length 73;
Best Local Similarity   100.0%;  Pred. No. 2.7e-65;
Matches  73;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy  1 MLLTLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1 MLLTLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60

Qy 61 AQPRGEGEKVGDG 73
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Db 61 AQPRGEGEKVGDG 73
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RESULT 6
US-10-011-833A-22
; Sequence 22, Application US/10011833A

; Patent No. 6951920
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C22
; CURRENT APPLICATION NUMBER: US/10/011,833A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-011-833A-22

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Query Match      100.0%;  Score 73;  DB 2;  Length 73;
Best Local Similarity   100.0%;  Pred. No. 2.7e-65;
Matches  73;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy  1 MLLTLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1 MLLTLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60

Qy 61 AQPRGEGEKVGDG 73
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Db 61 AQPRGEGEKVGDG 73
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RESULT 7
US-10-006-041A-22
; Sequence 22, Application US/10006041A
; Patent No. 6951921
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C8
; CURRENT APPLICATION NUMBER: US/10/006,041A

CURRENT FILING DATE: 2001-12-06
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 22
LENGTH: 73
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1-15
OTHER INFORMATION: Signal peptide.
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3-18
OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-006-041A-22

Query Match   100.0%; Score 73; DB 2; Length 73;
Best Local Similarity   100.0%; Pred. No. 2.7e-65;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLLTLLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFPPPSFLCLLPHRPAMTCSQ 60

Qy   61 AQPRGEGEKVGDG 73
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Db   61 AQPRGEGEKVGDG 73

RESULT 8
US-10-012-064A-22
Sequence 22, Application US/10012064A
Patent No. 6953841
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan 1.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
    Acids Encoding the Same
FILE REFERENCE: P2830P1C19
CURRENT APPLICATION NUMBER: US/10/012,064A
CURRENT FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098821
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/099536
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598

PRIOR FILING DATE: 1998-09-09
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 22
LENGTH: 73
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1-15
OTHER INFORMATION: Signal peptide.
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3-18
OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-012-064A-22

Query Match   100.0%; Score 73; DB 2; Length 73;
Best Local Similarity   100.0%; Pred. No. 2.7e-65;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLLTLLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFPPPSFLCLLPHRPAMTCSQ 60
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Db   1 MLLLTLLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFPPPSFLCLLPHRPAMTCSQ 60

Qy   61 AQPRGEGEKVGDG 73
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Db   61 AQPRGEGEKVGDG 73

RESULT 9
US-10-015-392A-22
Sequence 22, Application US/10015392A
Patent No. 6972186
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan 1.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
    Acids Encoding the Same
FILE REFERENCE: P2830P1C58
CURRENT APPLICATION NUMBER: US/10/015,392A
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098821
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/099536
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598

RESULT 10
US-10-011-795B-22
; Sequence 22, Application US/10011795B
; Patent No. 7012131
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C25
; CURRENT APPLICATION NUMBER: US/10/011,795B
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-015-392A-22

Query Match   100.0%;   Score 73;   DB 2;   Length 73;
Best Local Similarity   100.0%;   Pred. No. 2.7e-65;
Matches   73;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy   61 AQPRGEGEKVGDG 73
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Db   61 AQPRGEGEKVGDG 73

RESULT 11
US-10-015-386A-22
; Sequence 22, Application US/10015386A
; Patent No. 7022498
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C55
; CURRENT APPLICATION NUMBER: US/10/015,386A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-011-795B-22

Query Match   100.0%;   Score 73;   DB 3;   Length 73;
Best Local Similarity   100.0%;   Pred. No. 2.7e-65;
Matches   73;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy   61 AQPRGEGEKVGDG 73
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Db   61 AQPRGEGEKVGDG 73

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Db          1 MLLLTLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60

Qy         61 AQPRGEGEKVGDG 73
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Db         61 AQPRGEGEKVGDG 73
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RESULT 12
US-10-012-121A-22

; Sequence 22, Application US/10012121A
; Patent No. 7022817
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C20
; CURRENT APPLICATION NUMBER: US/10/012,121A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER:
; Prior Application removed - See File Wrapper or Palm
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; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-012-121A-22

Query Match   100.0%; Score 73; DB 3; Length 73;
Best Local Similarity   100.0%; Pred. No. 2.7e-65;
Matches   73; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy         61 AQPRGEGEKVGDG 73
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Db         61 AQPRGEGEKVGDG 73
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RESULT 13
US-10-006-485A-22

; Sequence 22, Application US/10006485A
; Patent No. 7026448
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C9
; CURRENT APPLICATION NUMBER: US/10/006,485A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
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; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
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~ PRIOR FILING DATE: 1998-09-17
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~ PRIOR FILING DATE: 1998-10-02
~ PRIOR APPLICATION NUMBER: 60/102965
~ PRIOR FILING DATE: 1998-10-06
~ PRIOR APPLICATION NUMBER: 60/103258
~ PRIOR FILING DATE: 1998-10-07
~ PRIOR APPLICATION NUMBER: 60/103314

~ PRIOR APPLICATION NUMBER: 60/103315
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~ PRIOR APPLICATION NUMBER: 60/106023
~ PRIOR FILING DATE: 1998-10-28

RESULT 14
US-10-006-746A-22
Sequence 22, Application US/10006746A
Patent No. 7026449
GENERAL INFORMATION:
~ APPLICANT: Baker, Kevin P.
~ APPLICANT: Botstein, David
~ APPLICANT: Desnoyers, Luc
~ APPLICANT: Eaton, Dan 1.
~ APPLICANT: Ferrara, Napoleone
~ APPLICANT: Fong, Sherman
~ APPLICANT: Gao, Wei-Qiang
~ APPLICANT: Goddard, Audrey

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Qy    1 MLLTLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60
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Qy   61 AQPRGEGEKVGDG 73
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Db   61 AQPRGEGEKVGDG 73
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Query Match   100.0%;   Score 73;   DB 3;   Length 73;
Best Local Similarity   100.0%;   Pred. No. 2.7e-65;
Matches 73;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1CS
CURRENT APPLICATION NUMBER: US/10/006,746A
CURRENT FILING DATE: 2001-12-06

PRIOR APPLICATION NUMBER: 60/098716
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PRIOR APPLICATION NUMBER: 60/098723
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PRIOR APPLICATION NUMBER: 60/103328
PRIOR FILING DATE: 1998-10-07

RESULT 15
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; Sequence 22, Application US/10012752A
; Patent No. 7026455
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C24
; CURRENT APPLICATION NUMBER: US/10/012,752A
; CURRENT FILING DATE: 2002-06-25
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-012-752A-22

Query Match   100.0%; Score 73; DB 3; Length 73;
Best Local Similarity   100.0%; Pred. No. 2.7e-65;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLITLLLLILLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLITLLLLILLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60

Qy   61 AQPRGEGEKVGDG 73
         |||||||||||||
Db   61 AQPRGEGEKVGDG 73

Search completed: June 6, 2006, 21:16:07
Job time : 51 secs

; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
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; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

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OM protein - protein search, using sw model

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                        GenCore version 5.1.9
                        Copyright (c) 1993 - 2006  Bioacceleration Ltd.

Run on:                 June   6, 2006, 21:06:23 ; Search time 293 seconds
                                                   (without alignments)
                                                   230.465 Million cell updates/sec

Title:                  US-10-063-534-30
Perfect score:          73
Sequence:               1 MLLLTLLLLLLLKGSCLEWL..........PAMTCSQAQPRGEGEKVGDG 73

Scoring table:          OLIGO
                        Gapop 60.0 , Gapext 60.0

Searched:               2849598 seqs, 925015592 residues

Word size :.            6

Total number of hits satisfying chosen parameters:       13623

Minimum DB seq length:  0
Maximum DB seq length:  2000000000

Post-processing: Listing first 45 summaries

Database :              UniProt_7.2:*
                        1: uniprot_sprot:*
                        2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                        SUMMARIES

Result              %     Query
No.    Score    Match  Length  DB  ID              Description
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  1    73     100.0    73      2   Q6UWT3_HUMAN    homo sapien
  2    13.7   13.7     337     2   Q3YP30_UTAST    uta stansbu
  3    13.7   13.7     338     2   Q3YP29_UTAST    uta stansbu
  4    13.7   13.7     341     2   Q3YP32_UTAST    uta stansbu
  5    13.7   13.7     343     2   Q3YP31_UTAST    uta stansbu
  6    13.7   13.7     347     2   Q3YP37_UTAST    uta stansbu
  7    13.7   13.7     379     1   CYB_BRAID       brachylagus
  8    10     13.7     418     1   Q3UNC6_MOUSE    mus musculu
  9    10     13.7     689     1   S27A5_MOUSE     m bile acyl
 10    10     12.3     39      2   Q5R588_PONPY    pongo pygma
 11    9      12.3     52      2   Q4X6W7_PLACH    plasmodium
 12    9      12.3     61      2   Q3R079_XYLFA    xylella fas
 13    9      12.3     75      2   Q8K4W3_MOUSE    mus musculu
 14    9      12.3     96      1   Q7NE75_GLOVI    gloeobacter
 15    9      12.3     99      1   Q8MKI6_BOVIN    bos taurus
 16    9      12.3     116     2   Q9EMP1_AMEPV    amsacta moo
 17    9      12.3     125     2   Q6IKC7_DROME    drosophila
 18    9      12.3     131     1   O43612_HUMAN    homo sapien
 19    9      12.3     131     1   OREX_PIG        sus scrofa
 20    9      12.3     133     2   O5UGI5_HUMAN    homo sapien
 21    9      12.3     146     2   O2KSD5_ADE04    human adeno
 22    9      12.3     152     2   O7R117_GIALA    giardia lam
 23    9      12.3     159     2   O5S9SC1_CANAL   candida alb
 24    9      12.3     161     2   Q4ALY9_CHLRB    chlorobium
 25    9      12.3     182     2   Q3GK41_CHLVI    prosthecoch
 26    9      12.3     184     2   O5S9SF3_CANAL   candida alb
 27    9      12.3     189     2   O8BLE9_MOUSE    mus musculu
 28    9      12.3     199     2   Q8IWY1_HUMAN    homo sapien
 29    9      12.3     200     2   Q496B3_HUMAN    homo sapien
 30    9      12.3     208     1   YHHN_ECO57      escherichia
 31    9      12.3     208     1   YHHN_ECOL6      escherichia
 32    9      12.3     208     1   YHHN_ECOLI      escherichia
 33    9      12.3     208     1   YHHN_SHIFL      shigella fl
 34    9      12.3     208     2   Q31VF8_SHIBS    shigella bo
 35    9      12.3     208     2   Q3YW60_SHISS    shigella so
 36    9      12.3     208     2   Q2M7D1_ECOLI    escherichia
 37    9      12.3     230     2   Q54UQ3_DICDI    dictyosteli
 38    9      12.3     235     2   Q8BJ86_MOUSE    mus musculu
 39    9      12.3     235     2   Q9D710_MOUSE    mus musculu
 40    9      12.3     236     2   Q4TEX9_TETNG    tetraodon n
 41    9      12.3     261     2   Q91237_MOUSE    m adult mal
 42    9      12.3     311     2   Q8IWY2_HUMAN    homo sapien
 43    9      12.3     313     2   Q86YW5_HUMAN    homo sapien
 44    9      12.3     381     2   Q30428_CANFA    canis famil
 45    9      12.3     382     2   Q9LHW0_ORYSA    oryza sativ
```

                                        ALIGNMENTS

RESULT 1
Q6UWT3_HUMAN

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ID   Q6UWT3_HUMAN    PRELIMINARY;    PRT;    73 AA.
AC   Q6UWT3;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   APELIN.
GN   ORFNames=UNQ471;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schonfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RL   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; AY358657; AAQ89020.1; -; mRNA.
SQ   SEQUENCE   73 AA;   7879 MW;  A99C96797BC4D91 CRC64;

Query Match             100.0%;  Score 73;  DB 2;  Length 73;
Best Local Similarity   100.0%;
  Matches   73;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLLLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60

Qy         61 AQPRGEGEKVGDG 73
              |||||||||||||
Db         61 AQPRGEGEKVGDG 73
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RESULT 2
Q3YP30_UTAST

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ID   Q3YP30_UTAST    PRELIMINARY;    PRT;    337 AA.
AC   Q3YP30;
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DT   27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   27-SEP-2005, sequence version 1.
DT   07-FEB-2006, entry version 6.
GN   Name=cytb;
DE   Cytochrome b (Fragment).
OS   Uta stansburiana (Side-blotched lizard).
OC   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae; Uta.
OX   NCBI_TaxID=43653;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ROM 37152;
RA   Lindell J., Murphy R.W.;
RT   "Simple identification of divergent mtDNA haplotypes with MAMA.";
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC   complex (complex III or cytochrome b-c1 complex), which is a
CC   respiratory chain that generates an electrochemical potential
CC   coupled to ATP synthesis (By similarity).
CC   -!- COFACTOR: Binds 2 heme groups noncovalently (By similarity).
CC   -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC   cytochrome c1 and the Rieske protein (By similarity).
CC   -!- SIMILARITY: Belongs to the cytochrome b family.
CC   ---
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---
DR   EMBL; DQ001863; AAZ20708.1; -; Genomic_DNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR   GO; GO:0005739; C:mitochondrion; IEA.
DR   GO; GO:0005506; F:iron ion binding; IEA.
DR   GO; GO:0046872; F:metal ion binding; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR005797; Cytb_b6_C.
DR   InterPro; IPR005798; Cytb_b6_N.
DR   Pfam; PF00032; Cytochrom_B_C; 1.
DR   Pfam; PF00033; Cytochrom_B_N; 1.
DR   PROSITE; PS51003; CYTB_CTER; 1.
DR   PROSITE; PS51002; CYTB_NTER; 1.
KW   Electron transport; Heme; Iron; Membrane; Metal-binding;
KW   Mitochondrion; Respiratory chain; Transmembrane; Transport.
FT   NON_TER   1   1
SQ   SEQUENCE   337 AA; 38057 MW; 63C33F43B2B58B35 CRC64;

Query Match   13.7%; Score 10; DB 2; Length 337;
Best Local Similarity   100.0%;
Matches   10; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 LLLTLLLLLL 11
                ||||||||||
Db   191 LLLTLLLLLL 200

RESULT 3
ID   Q3YP29_UTAST   PRELIMINARY;   PRT;   338 AA.
AC   Q3YP29;
DT   27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   27-SEP-2005, sequence version 1.
DT   07-FEB-2006, entry version 6.
GN   Name=cytb;
DE   Cytochrome b (Fragment).
OS   Uta stansburiana (Side-blotched lizard).
OC   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae; Uta.
OX   NCBI_TaxID=43653;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ROM 37151;

RC   STRAIN=ROM 37123;
RA   Lindell J., Murphy R.W.;
RT   "Simple identification of divergent mtDNA haplotypes with MAMA.";
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC   complex (complex III or cytochrome b-c1 complex), which is a
CC   respiratory chain that generates an electrochemical potential
CC   coupled to ATP synthesis (By similarity).
CC   -!- COFACTOR: Binds 2 heme groups noncovalently (By similarity).
CC   -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC   cytochrome c1 and the Rieske protein (By similarity).
CC   -!- SIMILARITY: Belongs to the cytochrome b family.
CC   ---
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---
DR   EMBL; DQ001864; AAZ20709.1; -; Genomic_DNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR   GO; GO:0005739; C:mitochondrion; IEA.
DR   GO; GO:0005506; F:iron ion binding; IEA.
DR   GO; GO:0046872; F:metal ion binding; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR005797; Cytb_b6_C.
DR   InterPro; IPR005798; Cytb_b6_N.
DR   Pfam; PF00032; Cytochrom_B_C; 1.
DR   Pfam; PF00033; Cytochrom_B_N; 1.
DR   PROSITE; PS51003; CYTB_CTER; 1.
DR   PROSITE; PS51002; CYTB_NTER; 1.
KW   Electron transport; Heme; Iron; Membrane; Metal-binding;
KW   Mitochondrion; Respiratory chain; Transmembrane; Transport.
FT   NON_TER   1   1
SQ   SEQUENCE   338 AA; 37974 MW; 4B90EC68A5D5B2AD CRC64;

Query Match   13.7%; Score 10; DB 2; Length 338;
Best Local Similarity   100.0%;
Matches   10; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 LLLTLLLLLL 11
                ||||||||||
Db   192 LLLTLLLLLL 201

RESULT 4
ID   Q3YP32_UTAST   PRELIMINARY;   PRT;   341 AA.
AC   Q3YP32;
DT   27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   27-SEP-2005, sequence version 1.
DT   07-FEB-2006, entry version 6.
GN   Name=cytb;
DE   Cytochrome b (Fragment).
OS   Uta stansburiana (Side-blotched lizard).
OC   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae; Uta.
OX   NCBI_TaxID=43653;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ROM 37151;
RA   Lindell J., Murphy R.W.;
RT   "Simple identification of divergent mtDNA haplotypes with MAMA.";
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC   complex (complex III or cytochrome b-c1 complex), which is a
CC   respiratory chain that generates an electrochemical potential
CC   coupled to ATP synthesis (By similarity).
CC   -!- COFACTOR: Binds 2 heme groups noncovalently (By similarity).
CC   -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC   cytochrome c1 and the Rieske protein (By similarity).
CC   -!- SIMILARITY: Belongs to the cytochrome b family.

```
CC   -----------------------------------------------------------------------
```
```
CC   -----------------------------------------------------------------------
DR   EMBL; DQ001861; AAZ20706.1; -; Genomic_DNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR   GO; GO:0005739; C:mitochondrion; IEA.
DR   PROSITE; PS51003; CYTB_NTER; 1.
DR   PROSITE; PS51002; CYTB_CTER; 1.
DR   GO; GO:0005506; F:iron ion binding; IEA.
DR   GO; GO:0046872; F:metal ion binding; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR005798; Cytb_b6_C.
DR   InterPro; IPR005797; Cytb_b6_N.
DR   Pfam; PF00032; Cytochrom_B_C; 1.
DR   Pfam; PF00033; Cytochrom_B_N; 1.
DR   PROSITE; PS51003; CYTB_NTER; 1.
DR   PROSITE; PS51002; CYTB_CTER; 1.
KW   Electron transport; Heme; Iron; Membrane; Metal-binding;
KW   Mitochondrion; Respiratory chain; Transmembrane; Transport.
FT   NON_TER       1      1
SQ   SEQUENCE   341 AA;  38482 MW;  0C25033BD9EC675D CRC64;

Query Match        13.7%;  Score 10;  DB 2;  Length 341;
Best Local Similarity  100.0%;  Pred. No. 0.94;
Matches  10;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy        2 LLLTLLLLLL 11
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Db      195 LLLTLLLLLL 204
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RESULT 5
Q3YP31_UTAST
ID   Q3YP31_UTAST            PRELIMINARY;     PRT;    343 AA.
AC   Q3YP31;
DT   27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   27-SEP-2005, sequence version 1.
DT   07-FEB-2006, entry version 6.
DE   Cytochrome b (Fragment).
GN   Name=cytb;
OS   Uta stansburiana (Side-blotched lizard).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae; Uta.
OX   NCBI_TaxID=43653;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ROM 37122;
RA   Lindell J., Murphy R.W.;
RT   "Simple identification of divergent mtDNA haplotypes with MAMA.";
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC       complex (complex III or cytochrome b-c1 complex), which is a
CC       respiratory chain that generates an electrochemical potential
CC       coupled to ATP synthesis (By similarity).
CC   -!- COFACTOR: Binds 2 heme groups noncovalently (By similarity).
CC   -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC       cytochrome c1 and the Rieske protein (By similarity).
CC   -!- SIMILARITY: Belongs to the cytochrome b family.
CC   -----------------------------------------------------------------------
```
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CC   -----------------------------------------------------------------------
DR   EMBL; DQ001862; AAZ20707.1; -; Genomic_DNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR   GO; GO:0005739; C:mitochondrion; IEA.
DR   GO; GO:0005506; F:iron ion binding; IEA.
DR   GO; GO:0046872; F:metal ion binding; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR005798; Cytb_b6_C.
DR   InterPro; IPR005797; Cytb_b6_N.
DR   Pfam; PF00032; Cytochrom_B_C; 1.
DR   Pfam; PF00033; Cytochrom_B_N; 1.
DR   PROSITE; PS51003; CYTB_NTER; 1.
DR   PROSITE; PS51002; CYTB_CTER; 1.
KW   Electron transport; Heme; Iron; Membrane; Metal-binding;
KW   Mitochondrion; Respiratory chain; Transmembrane; Transport.
FT   NON_TER       1      1
SQ   SEQUENCE   343 AA;  38755 MW;  9045C18C0B1ECC27 CRC64;

Query Match        13.7%;  Score 10;  DB 2;  Length 343;
Best Local Similarity  100.0%;  Pred. No. 0.95;
Matches  10;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy        2 LLLTLLLLLL 11
            ||||||||||
Db      197 LLLTLLLLLL 206
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RESULT 6
Q3YP37_UTAST
ID   Q3YP37_UTAST            PRELIMINARY;     PRT;    347 AA.
AC   Q3YP37;
DT   27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   27-SEP-2005, sequence version 1.
DT   07-FEB-2006, entry version 6.
DE   Cytochrome b (Fragment).
GN   Name=cytb;
OS   Uta stansburiana (Side-blotched lizard).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae; Uta.
OX   NCBI_TaxID=43653;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ROM 37048;
RA   Lindell J., Murphy R.W.;
RT   "Simple identification of divergent mtDNA haplotypes with MAMA.";
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC       complex (complex III or cytochrome b-c1 complex), which is a
CC       respiratory chain that generates an electrochemical potential
CC       coupled to ATP synthesis (By similarity).
CC   -!- COFACTOR: Binds 2 heme groups noncovalently (By similarity).
CC   -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC       cytochrome c1 and the Rieske protein (By similarity).
CC   -!- SIMILARITY: Belongs to the cytochrome b family.
CC   -----------------------------------------------------------------------
```
```
CC   -----------------------------------------------------------------------
DR   EMBL; DQ001855; AAZ20701.1; -; Genomic_DNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR   GO; GO:0005739; C:mitochondrion; IEA.
DR   GO; GO:0005506; F:iron ion binding; IEA.
DR   GO; GO:0046872; F:metal ion binding; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR005798; Cytb_b6_C.
DR   InterPro; IPR005797; Cytb_b6_N.
DR   Pfam; PF00032; Cytochrom_B_C; 1.
DR   Pfam; PF00033; Cytochrom_B_N; 1.
DR   PROSITE; PS51003; CYTB_NTER; 1.
DR   PROSITE; PS51002; CYTB_CTER; 1.
KW   Electron transport; Heme; Iron; Membrane; Metal-binding;
KW   Mitochondrion; Respiratory chain; Transmembrane; Transport.
FT   NON_TER       1      1
SQ   SEQUENCE   347 AA;  39075 MW;  D82F2642375D80BA CRC64;
```

Qy   2 LLLTLLLLLL 11
          |||||||||||
Db   201 LLLTLLLLLL 210

Query Match   13.7%; Score 10; DB 2; Length 347;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
CYB_BRAID
ID   CYB_BRAID   STANDARD;   PRT;   379 AA.
AC   Q6ELW3;
DT   15-MAR-2005, integrated into UniProtKB/Swiss-Prot.
DT   16-AUG-2004, sequence version 1.
DT   07-FEB-2006, entry version 16.
DE   Cytochrome b.
GN   Name=MT-CYB; Synonyms=COB, CYTB, MTCYB;
OS   Brachylagus idahoensis (Pygmy rabbit).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC   Brachylagus.
OX   NCBI_TaxID=48083;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   PubMed=15503672; DOI=10.1080/10635150490445715;
RA   Matthee C.A., van Vuuren B.J., Bell D., Robinson T.J.;
RT   "A molecular supermatrix of the rabbits and hares (Leporidae) allows
RT   for the identification of five intercontinental exchanges during the
RT   Miocene.";
RL   Syst. Biol. 53:433-447(2004).
CC   -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC   complex (complex III or cytochrome b-c1 complex), which is a
CC   respiratory chain that generates an electrochemical potential
CC   coupled to ATP synthesis (By similarity).
CC   -!- COFACTOR: Binds 2 heme groups noncovalently (By similarity).
CC   -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC   cytochrome c1 and the Rieske protein (By similarity).
CC   -!- MISCELLANEOUS: Heme 1 (or BL or b562) is low-potential and absorbs
CC   at about 562 nm, and heme 2 (or BH or b566) is high-potential and
CC   absorbs at about 566 nm (By similarity).
CC   -!- SIMILARITY: Belongs to the cytochrome b family.
DR   EMBL; AY292721; AAS54917.1; -; Genomic_DNA.
DR   SMR; Q6ELW3; 2-379.
DR   InterPro; IPR005798; Cytb_b6_C.
DR   InterPro; IPR005797; Cytb_b6_N.
DR   Pfam; PF00032; Cytochrom_B_C; 1.
DR   Pfam; PF00033; Cytochrom_B_N; 1.
DR   PROSITE; PS51003; CYTB_CTER; 1.
DR   PROSITE; PS51002; CYTB_NTER; 1.
KW   Electron transport; Heme; Iron; Membrane; Metal-binding; Transport;
KW   Mitochondrion; Respiratory chain; Transmembrane; Transport.
FT   CHAIN   1   379   Cytochrome b.
FT   /FTId=PRO_0000060690.
FT   METAL   83   83   Iron 1 (heme b562 axial ligand).
FT   METAL   97   97   Iron 2 (heme b566 axial ligand).
FT   METAL   182   182   Iron 1 (heme b562 axial ligand).
FT   METAL   196   196   Iron 2 (heme b566 axial ligand).
SQ   SEQUENCE   379 AA; 42755 MW; 9183997739658473 CRC64;

Qy   2 LLLTLLLLLL 11
          |||||||||||
Db   233 LLLTLLLLLL 242

Query Match   13.7%; Score 10; DB 1; Length 379;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
Q3UNC6_MOUSE
ID   Q3UNC6_MOUSE   PRELIMINARY;   PRT;   418 AA.
AC   Q3UNC6;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Adult male gall bladder cDNA, RIKEN full-length enriched library,
DE   clone:G630012H08 product:solute carrier family 27 (fatty acid
DE   transporter), member 5, full insert sequence.
GN   Name=Slc27a5;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Gall bladder;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Gall bladder;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Gall bladder;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   (Genome Network Core Team) and the Genome Science Group
RG   RIKEN Genome Exploration Research Group and the FANTOM Consortium;

RESULT 9

ID   S27A5_MOUSE   STANDARD;   PRT;   689 AA.
AC   Q4LDG0; O88694; Q91VD5;
DT   22-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT   22-NOV-2005, sequence version 2.
DT   07-MAR-2006, entry version 11.
DE   Bile acyl-CoA synthetase (EC 6.2.1.7) (BACS) (Bile acid CoA ligase)
DE   (BA-CoA ligase) (BAL) (Cholate--CoA ligase) (Very long chain acyl-CoA
DE   synthetase-related protein) (VLACS-related) (VLACSR) (Fatty acid
DE   transport protein 5) (FATP-5) (Solute carrier family 27 member 5).
GN   Name=Slc27a5; Synonyms=Acsb, Acsvl6, Fatp5, Vlacsr;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=BALB/c; TISSUE=Liver;
RX   MEDLINE=98308102; PubMed=9642112; DOI=10.1006/bbrc.1998.8770;
RA   Berger J., Truepe C., Neuman H., Forss-Petter S.;
RT   "A novel relative of the very-long-chain acyl-CoA synthetase and fatty
RT   acid transporter protein genes with a distinct expression pattern.";
RL   Biochem. Biophys. Res. Commun. 247:255-260(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC   STRAIN=C57BL/6J; TISSUE=Gall bladder;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).

RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Gall bladder;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).

RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Gall bladder;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Qy   4 LTILILLLLL 13
         ||||||||||
Db   7 LTILILLLLL 16

Query Match   13.7%; Score 10; DB 2; Length 418;
Best Local Similarity   100.0%; Pred. No. 1.1;
Matches   10; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

SQ   SEQUENCE   418 AA;   45626 MW; C05738017FAFA781 CRC64;

DR   EMBL; AK144301; BAE25821.1; -; mRNA.
DR   MGI; MGI:1347100; Slc27a5.
DR   GO; GO:0005783; C:endoplasmic reticulum; TAS.
DR   GO; GO:0005624; C:membrane; RCA.
DR   GO; GO:0003824; F:catalytic activity; RCA.
DR   GO; GO:0004467; F:long-chain-fatty-acid-CoA ligase activity; TAS.
DR   GO; GO:0016874; F:ligase activity; RCA.
DR   GO; GO:0001676; P:long-chain fatty acid metabolism; TAS.
DR   GO; GO:0008152; P:metabolism; RCA.
DR   InterPro; IPR000873; AMP-bind.
DR   PRINTS; PR00154; AMPBINDING.
DR   PROSITE; PS00455; AMP_BINDING; 1.

CC   -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC   family.
CC   ---
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---

RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
RT   Genome Res. 10:1757-1771(2000).
RT   sequencing pipeline with 384 multicapillary sequencer.";
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RA   Muramatsu M., Hayashizaki Y.;
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Hori F., Iida J., Imamura K., Itoh M., Kanagawa S.,
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Gall bladder;

RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka Y., Matsuura S., Kawai J.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

```
RC   STRAIN=FVB/N; TISSUE=Salivary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 28-689.
RX   MEDLINE=98337965; PubMed=9671728; DOI=10.1073/pnas.95.15.8625;
RA   Hirsch D., Stahl A., Lodish H.F.;
RT   "A family of fatty acid transporters conserved from mycobacterium to
RT   man.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:8625-8629(1998).
RN   [4]
RP   TISSUE SPECIFICITY.
RX   PubMed=11980911; DOI=10.1074/jbc.M203295200;
RA   Mihalik S.J., Steinberg S.J., Pei Z., Park J., Kim do G.,
RA   Heinzer A.K., Dacremont G., Wanders R.J., Cuebas D.A., Smith K.D.,
RA   Watkins P.A.;
RT   "Participation of two members of the very long-chain acyl-CoA
RT   synthetase family in bile acid synthesis and recycling.";
RL   J. Biol. Chem. 277:24771-24779(2002).
CC   -!- FUNCTION: Acyl-CoA synthetase involved in bile acid metabolism.
CC       Proposed to catalyze the first step in the conjugation of C24 bile
CC       acids (cholanoates) to glycine and taurine before excretion into
CC       bile canaliculi by activating them to their CoA thioesters. Seems
CC       to activate secondary bile acids entering the liver from the
CC       enterohepatic circulation (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + cholate + CoA = AMP + diphosphate +
CC       choloyl-CoA.
CC   -!- CATALYTIC ACTIVITY: ATP + (25R)-3-alpha,7-alpha,12-alpha-
CC       trihydroxy-5-beta-cholestan-26-oate + CoA = AMP + diphosphate +
CC       (25R)-3-alpha,12-alpha,7-alpha-trihydroxy-5-beta-cholestanoyl-CoA.
CC   -!- SUBCELLULAR LOCATION: Endoplasmic reticulum; endoplasmic reticulum
CC       membrane; multi-pass membrane protein (By similarity).
CC   -!- TISSUE SPECIFICITY: In liver expressed in a periportal
CC       distribution.
CC   -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC       family.
```

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DR   EMBL; AJ223959; CAA11688.1; -; mRNA.
DR   EMBL; BC013335; AAH13335.1; -; mRNA.
DR   EMBL; BC013272; AAH13272.1; -; mRNA.
DR   EMBL; AF072760; AAC40189.1; -; mRNA.
DR   PIR; JW0107; JW0107.
DR   Ensembl; ENSMUSG00000030382; Mus musculus.
DR   MGI; MGI:1347100; Slc27a5.
DR   GO; GO:0005783; C:endoplasmic reticulum; TAS.
DR   GO; GO:0005789; C:endoplasmic reticulum; TAS.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0004467; F:long-chain-fatty-acid-CoA ligase activity; TAS.
DR   GO; GO:0001676; P:long-chain fatty acid metabolism; TAS.
DR   InterPro; IPR000873; AMP-binding.
DR   Pfam; PF00501; AMP-binding; 1.
DR   PRINTS; PR00154; AMPBINDING.
DR   PROSITE; PS00455; AMP_BINDING; 1.
KW   ATP-binding; Endoplasmic reticulum; Fatty acid metabolism; Ligase;
KW   Lipid metabolism; Membrane; Nucleotide-binding; Transmembrane.
FT   CHAIN         1    689       Bile acyl-CoA synthetase.
FT                                /FTId=PRO_0000193214.
FT   TOPO_DOM      1      7       Cytoplasmic (By similarity).
FT   TRANSMEM      8     28       Potential.
FT   TRANSMEM     30     50       Potential.
FT   TRANSMEM     55     75       Potential.
FT   TOPO_DOM     76    689       Cytoplasmic (By similarity).
FT   NP_BIND     292    303       AMP (Potential).
FT   CONFLICT     88     88       K -> I (in Ref. 1).
FT   CONFLICT     88     88       K -> I (in Ref. 1).
FT   CONFLICT    408    408       K -> T (in Ref. 3).
FT   CONFLICT    568    568       C -> S (in Ref. 1).
FT   CONFLICT    568    568       C -> S (in Ref. 1).
FT   CONFLICT    688    688       N -> K (in Ref. 1).
SQ   SEQUENCE    689 AA;  76203 MW;  1642BBC2CF04FAA3 CRC64;

Qy   Query Match             13.7%;  Score 10;  DB 1;  Length 689;
     Best Local Similarity   100.0%;  Pred. No. 1.6;
     Matches   10;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy            4 LILLLLLLL 13
                |||||||||
Db            7 LILLLLLLL 16
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RESULT 10
Q5R588_PONPY
ID   Q5R588_PONPY            PRELIMINARY;       PRT;      39 AA.
AC   Q5R588;
DT   21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT   21-DEC-2004, sequence version 1.
DT   07-FEB-2006, entry version 6.
DE   Hypothetical protein DKFZp459K2327.
GN   Name=DKFZp459K2327.
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Cortex;
RG   The German cDNA Consortium;
RA   The German cDNA Consortium;
RA   Bloecker H., Boecker H., Brandt P., Mewes H.W., Weil B., Amid C.,
RA   Osanger A., Fobo G., Han M., Wiemann S.;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
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DR   EMBL; CR860976; CAH93078.1; -; mRNA.
DR   GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   PANTHER; PTHR11461; Prot_inh_serpin; 1.
KW   Hypothetical protein.
SQ   SEQUENCE    39 AA;   4116 MW;  1D796215B1C4D12 CRC64;

Qy   Query Match             12.3%;  Score 9;  DB 2;  Length 39;
     Best Local Similarity   100.0%;  Pred. No. 1.5;
     Matches    9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy            3 LILLLLLL 11
                ||||||||
Db            7 LILLLLLL 15
```

```
RESULT 11
Q4X6W7_PLACH
ID   Q4X6W7_PLACH            PRELIMINARY;       PRT;      52 AA.
AC   Q4X6W7;
DT   05-JUL-2005, integrated into UniProtKB/TrEMBL.
```

```
DT   05-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 4.
DE   Hypothetical protein.
OS   Plasmodium chabaudi.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5825;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15637271; DOI=10.1126/science.1103717;
RA   Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA   Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA   James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA   Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA   Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA   Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA   Sinden R.S.;
RT   "A comprehensive survey of the Plasmodium life cycle by genomic,
RT   transcriptomic, and proteomic analyses.";
RL   Science 307:82-86(2005).
```

```
DR   EMBL; CAA01009385; CAH87359.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   52 AA;   5868 MW;   447EAA6E9ECE9802 CRC64;

Query Match             12.3%;  Score 9;  DB 2;  Length 52;
Best Local Similarity   100.0%;  Pred. No. 1.8;
Matches    9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   6 LLLLLLLLK 14
        |||||||||
Db   9 LLLLLLLLK 17
```

```
RESULT 12
Q3R079_XYLFA
ID   Q3R079_XYLFA   PRELIMINARY;   PRT;   61 AA.
AC   Q3R079;
DT   25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   25-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Hypothetical protein precursor.
GN   ORFNames=XfasaDRAFT_0863;
OS   Xylella fastidiosa Ann-1.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC   Xanthomonadaceae; Xylella.
OX   NCBI_TaxID=155920;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RG   US DOE Joint Genome Institute (JGI_ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Xylella fastidiosa Ann-
RT   1.";
RL   Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome and assembly of Xylella fastidiosa
RT   Ann-1.";
RL   Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
```

```
RA   DOE Joint Genome Institute;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   STRAIN=Ann-1;
```

```
DR   EMBL; AAAM03000109; EAO30628.1; -; Genomic_DNA.
KW   Hypothetical protein; Signal.
FT   SIGNAL        1     47       Potential.
SQ   SEQUENCE   61 AA;   6846 MW;   3FB82714ECE41233 CRC64;

Query Match             12.3%;  Score 9;  DB 2;  Length 61;
Best Local Similarity   100.0%;  Pred. No. 2.1;
Matches    9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   5 LLLLLLLLL 13
        |||||||||
Db   8 LLLLLLLLL 16
```

```
RESULT 13
Q8K4W3_MOUSE
ID   Q8K4W3_MOUSE   PRELIMINARY;   PRT;   75 AA.
AC   Q8K4W3;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   Scotin (Fragment).
GN   Name=Scotin;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ICRxSwiss;
RX   MEDLINE=22131632; PubMed=12135983; DOI=10.1083/jcb.200203006;
RA   Bourdon J.C., Renzing J., Robertson P.L., Fernandes K.N., Lane D.P.;
RT   "Scotin, a novel p53-inducible proapoptotic protein located in the ER
RT   and the nuclear membrane.";
RL   J. Cell Biol. 158:235-246(2002).
```

```
DR   EMBL; AF520701; AAM74234.1; -; Genomic_DNA.
DR   EMBL; AF520700; AAM74234.1; JOINED; Genomic_DNA.
DR   Ensembl; ENSMUSG00000025647; Mus musculus.
DR   MGI; MGI:1915044; Scotin.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0016021; C:integral to membrane; IDA.
DR   GO; GO:0005635; C:nuclear envelope; RCA.
DR   GO; GO:0008632; P:apoptotic program; IDA.
DR   GO; GO:0006917; P:induction of apoptosis; IDA.
NON_TER       75     75
SQ   SEQUENCE   75 AA;   8253 MW;   DBB52F2072BE48AB CRC64;

Query Match             12.3%;  Score 9;  DB 2;  Length 75;
Best Local Similarity   100.0%;  Pred. No. 2.4;
Matches    9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   5 LLLLLLLLL 13
```

```
Db        |||||||||
       10 TLLLLLLL 18
```

RESULT 14

```
ID   Q7NE75_GLOVI      PRELIMINARY;    PRT;    96 AA.
AC   Q7NE75;
DT   15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT   15-DEC-2003, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Gsl4005 protein.
GN   OrderedLocusNames=gsl4005;
OS   Gloeobacter violaceus.
OC   Bacteria; Cyanobacteria; Gloeobacteria; Gloeobacterales; Gloeobacter.
OX   NCBI_TaxID=33072;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=PCC 7421;
RX   MEDLINE=22977040; PubMed=14621292; DOI=10.1093/dnares/10.4.137;
RA   Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
RA   Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA   Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
RA   Takeuchi C., Yamada M., Tabata S.;
RT   "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT   cyanobacterium that lacks thylakoids.";
RL   DNA Res. 10:137-145(2003).
```
```
DR   EMBL; BA000045; BAC91946.1; -; Genomic_DNA.
DR   BioCyc; GVIO251221:GSL4005-MONOMER; -.
KW   Complete proteome.
SQ   SEQUENCE   96 AA;  11018 MW;  1C2FF9643578492 CRC64;

Query Match             12.3%;  Score 9; DB 2; Length 96;
Best Local Similarity  100.0%;  Pred. No. 3;
Matches    9;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy       3  LILTLLLLL 11
            |||||||||
Db       2  LILTLLLLL 10
```

RESULT 15

```
ID   Q8MKI6_BOVIN      PRELIMINARY;    PRT;    99 AA.
AC   Q8MKI6;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   Prepro-orexin (Fragment).
GN   Name=BORX;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Watanabe K., Aso H., Sato T., Tahara K., Takano S., Yamaguchi T.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
```
```
DR   EMBL; AB084625; BAB91446.1; -; mRNA.
DR   Ensembl; ENSBTAG00000000665; Bos taurus.
DR   GO; GO:0007631; P:feeding behavior; IEA.
DR   GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
DR   InterPro; IPR001704; Orexin.
DR   PANTHER; PTHR15173; Orexin; 1.
DR   Pfam; PF02072; Orexin; 1.
DR   PRINTS; PR01091; OREXININPP.
FT   NON_TER    99    99
SQ   SEQUENCE   99 AA;  10372 MW;  8F9F5E6B9EB8AE5D CRC64;

Query Match             12.3%;  Score 9; DB 2; Length 99;
Best Local Similarity  100.0%;  Pred. No. 3;
Matches    9;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy       5  TLLLLLLL 13
            ||||||||
Db      14  TLLLLLLL 22

Search completed: June  6, 2006, 21:14:29
Job time : 296 secs
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OM protein - protein search, using sw model

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GenCore version 5.1.9

Run on: June 6, 2006, 21:09:48 ; Search time 38 Seconds
                 (without alignments)
                 184.837 Million cell updates/sec

Title: US-10-063-534-30
Perfect score: 73
Sequence: 1 MLLLTLLLLLLLKGSCLEW.............PAMTCSQAQPRGEBKVGDG 73

Scoring table: OLIGO
                 Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size :   6

Total number of hits satisfying chosen parameters: 1373

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   PIR_80:*
                 1: piri:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	10	13.7	689	1	JW0107	very-long-chain ac
2	9	12.3	208	2	E86014	probable enzyme yh
3	9	12.3	208	2	E91168	probable enzyme [i
4	9	12.3	208	2	S47687	hypothetical prote
5	9	12.3	381	2	S35940	class I histocompa
6	9	12.3	500	1	ITHUC1	complement C1 inhi
7	9	12.3	537	2	T49162	hypothetical prote
8	9	12.3	1894	2	JC4980	plexin 1 precursor
9	9	12.3	53	2	S05486	alpha-amylase [EC
10	8	11.0	77	2	A03982	p15E protein - sim
11	8	11.0	82	2	JQ1181	outer envelope mem
12	8	11.0	101	2	B28414	growth-regulated p
13	8	11.0	112	2	A60111	sporozoite antigen
14	8	11.0	131	2	P00059	T-cell receptor be
15	8	11.0	133	2	JC2202	secretin precursor
16	8	11.0	133	2	S57038	probable membrane
17	8	11.0	134	2	A40959	secretin precursor
18	8	11.0	135	2	C82176	hypothetical prote
19	8	11.0	144	2	T18867	hypothetical prote
20	8	11.0	171	2	S19502	hypothetical prote
21	8	11.0	174	2	I38063	neuromedin U precu
22	8	11.0	182	2	JC7236	receptor-activity-
23	8	11.0	185	2	A49957	CD45-associated 30
24	8	11.0	185	2	I40490	hypothetical prote
25	8	11.0	189	2	JC7262	receptor activity
26	8	11.0	197	2	S51372	membrane protein L
27	8	11.0	201	2	I38850	LERK-4 - human
28	8	11.0	205	2	S37804	hypothetical prote
29	8	11.0	206	2	S18250	collagen alpha 1(I
30	8	11.0	206	2	A55412	lymphocyte phospha
31	8	11.0	208	2	T06492	ribosomal protein
32	8	11.0	208	2	AC0991	probable membrane
33	8	11.0	208	2	AC0465	probable membrane
34	8	11.0	220	2	S43291	FLT3/FLK2 ligand (
35	8	11.0	220	1	I58343	flt3 ligand isofor
36	8	11.0	231	2	A49265	flt3/flk-2 ligand
37	8	11.0	244	2	S18948	centrocyclin precu
38	8	11.0	245	1	C1HUQC	complement subcomp
39	8	11.0	249	1	A25842	chymase (EC 3.4.21
40	8	11.0	259	2	A71537	probable n-acetylm
41	8	11.0	263	2	S57346	interleukin 15 rec
42	8	11.0	285	2	JC5639	1-acylglycerol-3-p
43	8	11.0	291	2	B60131	homeotic protein X
44	8	11.0	304	2	T02679	probable RNA-bindi
45	8	11.0	318	2	I59301	bone marrow stroma

ALIGNMENTS

RESULT 1
JW0107
very-long-chain acyl-CoA synthetase related protein - mouse
N;Alternate names: VLACSR
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JW0107
R;Berger, J.; Truppe, C.; Neumann, H.; Forss-Petter, S.
Biochem. Biophys. Res. Commun. 247, 255-260, 1998
A;Title: A novel relative of the very-long-chain acyl-CoA synthetase and fatty acid tran
A;Reference number: JW0107; MUID:98308102; PMID:9642112
A;Accession: JW0107
A;Molecule type: mRNA
A;Residues: 1-689 <BER>
A;Cross-references: UNIPROT:Q91VD5; UNIPARC:UPI000174C70; GB:AJ223959
A;Experimental source: liver
C;Comment: This protein likely functions as a plasma membrane transporter of long chain f
C;Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate-CoA ligase hom
F;169-647/Domain: acetate-CoA ligase homology <ACL>

Query Match   13.7%; Score 10; DB 1; Length 689;
Best Local Similarity   100.0%;
Matches   10; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   4 LTLLLLLLK 13
            |||||||||
Db   7 LTLLLLLLK 16

RESULT 2
E86014
probable enzyme yhhN [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: E86014
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E86014
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-208 <STO>
A;Cross-references: UNIPROT:P37616; UNIPARC:UPI0000165965; GB:AE005174; NID:g12518127; P
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yhhN
C;Superfamily: Escherichia coli hypothetical protein o208

Query Match   12.3%; Score 9; DB 2; Length 208;

```
Qy          4 LTLLLLLL 12
              |||||||||
Db         33 LTLLLLLL 41

RESULT 3
E91168
probable enzyme [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: E91168
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E91168
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-208 <HAY>
A;Cross-references: UNIPROT:P37616; UNIPARC:UPI00000013B251; GB;BA000007; PIDN:BAB37740.1;
C;Genetics:
C;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Gene: ECs4317
C;Superfamily: Escherichia coli hypothetical protein 0208

Query Match         12.3%;  Score 9;  DB 2;  Length 208;
Best Local Similarity  100.0%;
Matches        9;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          4 LTLLLLLL 12
              |||||||||
Db         33 LTLLLLLL 41

RESULT 4
S47687
hypothetical protein o208 - Escherichia coli (strain K-12)
N;Alternate names: hypothetical protein b3468
C;Species: Escherichia coli
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: S47687; G65143
R;Plunkett, G.
submitted to the EMBL Data Library, March 1994
A;Reference number: S47666
A;Accession: S47687
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-208 <PLU>
A;Cross-references: UNIPROT:P37616; UNIPARC:UPI00000013B251; EMBL:U00039; NID:g9465582; PID
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G65143
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-208 <BLAT>
A;Cross-references: UNIPARC:UPI00000013B251; GB;AE000422; GB;U00096; NID:g1789868; PIDN:AD
A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: Escherichia coli hypothetical protein o208

Query Match         12.3%;  Score 9;  DB 2;  Length 208;
Best Local Similarity  100.0%;
Matches        9;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          4 LTLLLLLL 12
              |||||||||
Db         33 LTLLLLLL 41
```

```
RESULT 5
S35940
class I histocompatibility antigen DLA-6.7B - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S35940
R;Burnett, R.C.
submitted to the EMBL Data Library, August 1993
A;Description: Molecular analysis of a canine MHC class Ib gene, DLA-6.7B.
A;Reference number: S35940
A;Accession: S35940
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-381 <BUR>
A;Cross-references: UNIPROT:Q30428; UNIPARC:UPI0000089557; EMBL:Z25418; NID:g396224; PID
C;Genetics:
A;Introns: 30/1; 121/1; 213/1; 305/1; 343/1; 359/1; 373/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;226-291;Domain: immunoglobulin homology <IMM>

Query Match         12.3%;  Score 9;  DB 2;  Length 381;
Best Local Similarity  100.0%;
Matches        9;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          5 TLLLLLLLL 13
              |||||||||
Db          8 TLLLLLLLL 16

RESULT 6
ITHUC1
complement C1 inhibitor precursor [validated] - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 05-Oct-2004
C;Accession: S15386; S00403; A38781; B38781; A24161; A38782; S03370; A34847; S15084; A24;
R;Carter, P.E.; Duponchel, C.; Tosi, M.; Fothergill, J.E.
Eur. J. Biochem. 197, 301-308, 1991
A;Reference number: S15386; MUID:91224119; PMID:2026152
A;Accession: S15386
A;Molecule type: DNA
A;Residues: 1-500 <CA2>
A;Cross-references: UNIPROT:P05155; UNIPARC:UPI000000123F; EMBL:X54486; NID:g929534; PIDN
R;Carter, P.E.; Dunbar, B.; Fothergill, J.E.
Eur. J. Biochem. 173, 163-169, 1988
A;Title: Genomic and cDNA cloning of the human C1 inhibitor. Intron-exon junctions and co
A;Reference number: S00403; MUID:88185313; PMID:3267220
A;Accession: S00403
A;Molecule type: DNA
A;Residues: 1-500 <CAR>
A;Cross-references: UNIPARC:UPI0000000123F; EMBL:X07427; NID:g929520; PIDN:CAA30314.1; PID
A;Residues: 178-500 <CA3>
A;Cross-references: UNIPARC:UPI000000016A617; GB;X07577; NID:g929536; PIDN:CAA30469.1; PID:gt
A;Accession: B38781
A;Molecule type: DNA
A;Residues: 173-237,'X',239-252,'X',254,'X',256-264,'X',266-268,277-286,330-333,335-340;
A;Cross-references: UNIPARC:UPI000000040C48; UNIPARC:UPI00000017318A;
1BF
A;Molecule type: protein
A;Residues: 1-186,'Q',188-500 <BOC>
R;Bock, S.C.; Skriver, K.; Nielsen, E.; Thøgersen, H.C.; Wiman, B.; Donaldson, V.H.; Eddy
Biochemistry 25, 4292-4301, 1986
A;Title: Human C1 inhibitor: primary structure, cDNA cloning, and chromosomal localizatio
A;Reference number: A24161; MUID:87000544; PMID:3756141
A;Accession: A24161
A;Molecule type: mRNA
A;Residues: 1-500 <BO2>
A;Cross-references: UNIPARC:UPI000145144; EMBL:M13656; NID:g179620; PIDN:AAB59387.1; PII
A;Accession: A38782
A;Molecule type: protein
A;Residues: 23-500 <B02>
```

```
Qy          4 LTLLLLLL 12
              |||||||||
Db         33 LTLLLLLL 41
```

A;Cross-references: UNIPARC:UPI00001731C0
A;Note: 480-Met was also found
R;Rauth, G.; Schumacher, G.; Buckel, P.; Mueller-Esterl, W.
Proc. Natl. Acad. Sci. U.S.A. 1, 251-257, 1988
Protein Seq. Data Anal. 1, 251-257, 1988
A;Title: Molecular cloning of the cDNA coding for human C1(-) inhibitor.
A;Reference number: S03370; MUID:88276848; PMID:3393514
A;Accession: S03370
A;Molecule type: mRNA
A;Residues: 'PPVQ',6-479,'M',481-500 <RAU>
A;Cross-references: UNIPARC:UPI00001731C1
A;Molecule type: DNA
A;Residues: 33-228 <STO>
A;Cross-references: UNIPARC:UPI00001731C2; GB:M30688
R;Que, B.G.
A;Gene: GDB:C1NH
submitted to the EMBL Data Library, November 1986
A;Reference number: S15084
A;Accession: S15084
A;Molecule type: mRNA
A;Residues: 1-305; R',307-500 <QUE>
A;Cross-references: UNIPARC:UPI00001731CE
Biochem. Biophys. Res. Commun. 137, 620-625, 1986
R;Que, B.G.; Petra, P.H.
A;Reference number: A34847; MUID:90160364; PMID:2154751
A;Accession: A34847
A;Molecule type: mRNA
A;Residues: 1-305; R',307-500 <QUE>
A;Cross-references: UNIPARC:UPI00001731CC; UNIPARC:UPI00001731CB; EMBL:M13690; NID:g179618; PIDN:AAA35613.1; PI
A;Title: Isolation and analysis of a cDNA coding for human C1 inhibitor.
A;Reference number: A24258; MUID:86268965; PMID:3488058
A;Accession: A24258
R;Tosi, M.; Duponchel, C.; Bourgarel, P.; Colomb, M.; Meo, T.
Gene 42, 265-272, 1986
A;Title: Molecular cloning of human C1 inhibitor: sequence homologies with alpha(1)-anti
A;Reference number: S15529; MUID:86276001; PMID:3089875
A;Accession: S15529
A;Molecule type: mRNA
A;Residues: 213-500 <TOS>
A;Cross-references: UNIPARC:UPI000016A614; EMBL:M14036; NID:g179616; PIDN:AAA51848.1; PI
R;Davis III, A.E.; Whitehead, A.S.; Harrison, R.A.; Dauphinais, A.; Bruns, G.A.P.; Cicar
Proc. Natl. Acad. Sci. U.S.A. 83, 3161-3165, 1986
A;Title: Human inhibitor of the first component of complement, C1: characterization of c
A;Reference number: A23936; MUID:86205856; PMID:3458172
A;Accession: A23936
A;Molecule type: mRNA
A;Residues: 241-314,'QLQKLSY',321,'M',323-331,'L',333-369,'TGTGSQ',376-416,'V',418-438,'
A;Cross-references: UNIPARC:UPI00001731C3; EMBL:M13690
A;Residues: 187,'K',189-408,413-500 <QU2>
A;Cross-references: UNIPARC:UPI00001731C4; EMBL:M13203
A;Note: the authors translated the codon CTG for residue 332 as Val
A;Accession: A38783
A;Molecule type: protein
A;Residues: 23-24,'X',26-47,'X',48-62 <HAR>
A;Cross-references: UNIPARC:UPI00001731CD
R;Salvesen, G.S.; Catanese, J.J.; Kress, L.F.; Travis, J.
J. Biol. Chem. 260, 2432-2436, 1985
A;Title: Primary structure of the reactive site of human C1-inhibitor.
A;Reference number: S15006; MUID:85130906; PMID:3519001
A;Accession: S15006
A;Molecule type: protein
A;Residues: 'I',61-62,'XX',65-68,464-475 <SAL>
A;Cross-references: UNIPARC:UPI00001731CC; UNIPARC:UPI00001731CD
R;Parad, R.B.; Kramer, J.; Strunk, R.C.; Rosen, F.S.; Davis III, A.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 6786-6790, 1990
A;Title: Dysfunctional C1 inhibitor Ta: deletion of Lys-251 results in acquisition of an

A;Reference number: A36053; MUID:90370868; PMID:2118657
A;Accession: A36053
A;Molecule type: protein
A;Residues: 266-282 <PAR>
A;Cross-references: GDB:119041; OMIM:106100
A;Map position: 11q12.1-11q13.1
A;Introns: 17/3; 184/1; 229/1; 297/1; 343/3; 417/1
C;Superfamily: serpin
C;Keywords: glycoprotein; serine proteinase inhibitor; tandem repeat
C;Comment: This protein inhibits the serine proteinase activity in complement factors C1
C;Comment: Defects in this protein result in hereditary angioneurotic edema. In type I d
C;Genetics:
A;Cross-references: GDB:119041; OMIM:106100
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-500/Product: complement C1 inhibitor #status predicted <MAT>
F;23-119/Domain: glycosylated #status predicted <GLC>
F;65-119/Region: 4-residue repeats
F;120-500/Domain: inhibitory #status predicted <INH>
F;25,69,81,238,253,352/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;48,71,83,88,92,96/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;64/Binding site: carbohydrate (Ser) (covalent) #status experimental
F;72,99,106,107,111,115,118,119/Binding site: carbohydrate (Thr) (covalent) #status pred
F;123-428,130-205/Disulfide bonds: #status experimental
F;466/Inhibitory site: Arg (complement C1) #status experimental

Qy　3 LLLLLLLLL 11
　　　||||||||||
Db　7 LLLLLLLLL 15

Query Match　　　12.3%;　Score 9;　DB 1;　Length 500;
Best Local Similarity　100.0%;　Pred. No. 0.87;
Matches　9;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

RESULT 7
T49162
hypothetical protein T20N10.140 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49162
R;D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.; Le
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25017
A;Accession: T49162
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-537 <DAN>
A;Cross-references: UNIPROT:Q9LXS3; UNIPARC:UPI00009F3C5; EMBL:AL353032; GSPDB:GN00061;
A;Experimental source: cultivar Columbia; BAC clone T20N10
C;Genetics:
A;Gene: ATSP:T20N10.140
A;Map position: 3
A;Introns: 80/1; 94/3; 150/3; 342/3; 443/3

Qy　5 TLLLLLLLL 13
　　　|||||||||
Db　45 TLLLLLLLL 53

Query Match　　　12.3%;　Score 9;　DB 2;　Length 537;
Best Local Similarity　100.0%;　Pred. No. 0.92;
Matches　9;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

RESULT 8
JC4980
plexin 1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 09-Jul-2004
C;Accession: JC4980
R;Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, H
Biochem. Biophys. Res. Commun. 226, 524-529, 1996

A;Title: Identification of a neuronal cell surface molecule, plexin, in mice.
A;Reference number: JC4980; MUID:96400291; PMID:8806667
A;Accession: JC4980
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1894 <KAM>
A;Cross-references: UNIPROT:P70206; UNIPARC:UPI0000023AE; DDBJ:D86948; NID:g1665756; PI
A;Experimental source: brain
C;Comment: This protein is a membrane protein, and plays a role in neuronal cell contact
sence of calcium ions.
C;Keywords: duplication; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;513-561,659-704,807-859/Region: cysteine-rich
F;1238-1264/Domain: transmembrane #status predicted <TMM>
F;1266-1268/Region: hydrophilic

Qy
Db

Query Match　　　　12.3%;　Score 9;　DB 2;　Length 1894;
Best Local Similarity　100.0%;　Pred. No. 2.5;
　　Matches　　9;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

Qy　　5 TLLLLLLLL 13
Db　　10 TLLLLLLLL 18

RESULT 9
S05486
alpha-amylase (EC 3.2.1.1) 2.34 precursor - wheat (fragment)
C;Species: Triticum aestivum (common wheat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 31-Dec-2004
C;Accession: S05486
R;Huttly, A.K.; Mattiessen, R.A.; Baulcombe, D.C.
Mol. Gen. Genet. 214, 232-240, 1988
A;Title: Sequence heterogeneity and differential expression of the alpha-Amy-2 gene fam
A;Reference number: S05486; MUID:89181522; PMID:2467183
A;Accession: S05486
A;Molecule type: DNA
A;Status: translation not shown
A;Residues: 1-53 <HUT>
A;Cross-references: UNIPARC:UPI0000A6FDC; EMBL:X13578; NID:g21662; PIDN
C;Genetics:
A;Gene: amy2
A;Map position: 7D
A;Introns: 32/3
C;Function:
A;Pathway: glycogen/starch degradation
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
C;Superfamily: alpha-amylase, plant type; alpha-amylase core homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Qy
Db

Query Match　　　　11.8%;　Score 8;　DB 2;　Length 53;
Best Local Similarity　100.0%;　Pred. No. 1.3;
　　Matches　　8;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

Qy　　6 LLLLLLLL 13
Db　　12 LLLLLLLL 19

RESULT 10
A03982
p15E protein - simian sarcoma virus (fragment)
C;Species: simian sarcoma virus
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: A03982
R;Devare, S.G.; Reddy, E.P.; Law, J.D.; Robbins, K.C.; Aaronson, S.A.
Proc. Natl. Acad. Sci. U.S.A. 80, 731-735, 1983
A;Title: Nucleotide sequence of the simian sarcoma virus genome: demonstration that its
A;Reference number: A03982; MUID:83144004; PMID:6298772
A;Accession: A03982
A;Molecule type: genomic RNA
A;Residues: 1-77 <DEV>
A;Cross-references: UNIPARC:UPI00012A05A; GB:V01201; GB:J02394; GB:J023

C;Genetics:
A;Gene: env
C;Superfamily: type C retrovirus env polyprotein

Qy
Db

Query Match　　　　11.0%;　Score 8;　DB 2;　Length 77;
Best Local Similarity　100.0%;　Pred. No. 1.7;
　　Matches　　8;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

Qy　　6 LLLLLLLL 13
Db　　31 LLLLLLLL 38

RESULT 11
JQ1181
outer envelope membrane 14K protein, chloroplast - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 19-Jan-1996
C;Accession: JQ1181
R;Li, H.M.; Moore, T.; Keegstra, K.
Plant Cell 3, 709-717, 1991
A;Title: Targeting of proteins to the outer envelope membrane uses a different pathway th
A;Reference number: JQ1181; MUID:93044506; PMID:1841725
A;Accession: JQ1181
A;Molecule type: mRNA
A;Residues: 1-82 <LIH>
A;Cross-references: UNIPARC:UPI0000017B068; GB:M69105
A;Experimental source: leaf, cv. Perfection
C;Keywords: chloroplast; membrane protein

Qy
Db

Query Match　　　　11.0%;　Score 8;　DB 2;　Length 82;
Best Local Similarity　100.0%;　Pred. No. 1.8;
　　Matches　　8;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

Qy　　7 LLLLLLLK 14
Db　　48 LLLLLLLK 55

RESULT 12
B28414
growth-regulated protein precursor - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: B28414
R;Anisowicz, A.; Bardwell, L.; Sager, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7188-7192, 1987
A;Title: Constitutive overexpression of a growth-regulated gene in transformed Chinese ha
A;Reference number: A94184; MUID:88041072; PMID:2890161
A;Accession: B28414
A;Molecule type: mRNA
A;Residues: 1-101 <ANI>
A;Cross-references: UNIPROT:P09340; UNIPARC:UPI000012BAF7; GB:J03560; NID:g191088; PIDN:l
A;Note: the authors translated the codon CAG for residue 52 as Glu
C;Superfamily: beta-thromboglobulin
F;1-23/Domain: signal sequence #status predicted protein #status predicted <MAT>
F;24-101/Product: growth-regulated protein #status predicted <SIG>

Qy
Db

Query Match　　　　11.0%;　Score 8;　DB 2;　Length 101;
Best Local Similarity　100.0%;　Pred. No. 2.1;
　　Matches　　8;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

Qy　　6 LLLLLLLL 13
Db　　13 LLLLLLLL 20

RESULT 13
A60111
sporozoite antigen - Eimeria tenella (fragment)
C;Species: Eimeria tenella
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 17-Jul-1994
C;Accession: A60111

R;Miller, G.A.; Bhogal, B.S.; McCandliss, R.; Strausberg, R.L.; Jessee, E.J.; Anderson,
Infect. Immun. 57, 2014-2020, 1989
A;Title: Characterization and vaccine potential of a novel recombinant coccidial antigen
A;Reference number: A60111; MUID:89277516; PMID:2659532
A;Accession: A60111
A;Molecule type: mRNA
A;Status: Preliminary
A;Residues: 1-112 <MIL>
A;Cross-references: UNIPARC:UPI000142143

Qy   6 LLLLLLLL 13
      |||||||||
Db   1 LLLLLLLL 8

Query Match   11.0%;   Score 8;   DB 2;   Length 112;
Best Local Similarity   100.0%;   Pred. No. 2.3;
Matches   8;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 14
PQ0059
T-cell receptor beta chain (BTB93) - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 30-May-1997
C;Accession: PQ0059
R;Tanaka, A.; Ishiguro, N.; Shinagawa, M.
submitted to JIPID, May 1990
A;Reference number: JQ0472
A;Description: Sequence analysis of bovine T-cell receptor beta chain genes.
A;Accession: PQ0059
A;Molecule type: mRNA
A;Residues: 1-131 <ACC>
A;Cross-references: UNIPARC:UPI000011D083
C;Genetics:
A;Gene: BTB93
A;Experimental source: T cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Qy   4 LLLLLLLL 11
      |||||||||
Db   2 LLLLLLLL 9

Query Match   11.0%;   Score 8;   DB 2;   Length 131;
Best Local Similarity   100.0%;   Pred. No. 2.6;
Matches   8;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 15
JC2202
secretin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C;Accession: JC2202; S34214
R;Lan, M.S.; Kajiyama, W.; Donadel, G.; Lu, J.; Notkins, A.L.
Biochem. Biophys. Res. Commun. 200, 1066-1071, 1994
A;Title: cDNA sequence and genomic organization of mouse secretin.
A;Reference number: JC2202; MUID:94234995; PMID:8179583
A;Accession: JC2202
A;Molecule type: mRNA
A;Residues: 1-133 <LAN>
A;Cross-references: UNIPROT:Q08535; UNIPARC:UPI000026321; EMBL:X73580; NID:g313710; PID
C;Comment: This protein regulates the secretion of pancreatic juices and stimulates insu
C;Superfamily: glucagon
C;Keywords: amidated carboxyl end; duplication; hormone; secretagogue
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-133/Product: prosecretin #status predicted <PRO>
F;32-58/Product: secretin #status predicted <MAT>
F;58/Modified site: amidated carboxyl end (Val) (amide in mature form from following gly

Query Match   11.0%;   Score 8;   DB 2;   Length 133;
Best Local Similarity   100.0%;   Pred. No. 2.6;
Matches   8;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   6 LLLLLLLL 13
      |||||||||
Db   10 LLLLLLLL 17

Search completed: June 6, 2006, 21:15:12
Job time : 40 secs

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OM protein - protein search, using sw model

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GenCore version 5.1.9

Run on: June 6, 2006, 21:51:09 ; Search time 16 Seconds (without alignments)
52.766 Million cell updates/sec

Title: US-10-063-534-30
Perfect score: 386
Sequence: 1 MLLLTLLLLLLLLKGSCLEW.........PAMTCSQAQPRGEGEKVGDG 73

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SID53/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SID53/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SID53/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SID53/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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8: /EMC_Celerra_SID53/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	386	100.0	73	7	US-11-101-316-30	Sequence 30, Appl
2	63	16.3	124	6	US-10-511-455-23	Sequence 23, Appl
3	62.5	16.2	86	6	US-10-511-455-25	Sequence 25, Appl
4	59	15.3	91	6	US-10-511-455-17	Sequence 17, Appl
5	59	15.3	142	6	US-10-511-937-2432	Sequence 2432, Ap
6	59	15.3	468	6	US-10-953-349-10909	Sequence 10909, A
7	59	15.3	469	6	US-10-953-349-10908	Sequence 10908, A
8	59	15.3	503	6	US-10-953-349-10907	Sequence 10907, A
9	58.5	15.2	155	6	US-10-953-349-35222	Sequence 35222, A
10	58	15.0	432	6	US-10-196-749-74	Sequence 74, Appl
11	57.5	14.9	166	6	US-10-953-349-35817	Sequence 35817, A
12	57.5	14.9	215	6	US-10-953-349-35815	Sequence 35815, A
13	57	14.8	208	6	US-10-953-349-15677	Sequence 15677, A
14	56	14.5	864	7	US-11-312-797-2	Sequence 2, Appli
15	56	14.5	85	6	US-11-312-797-27987	Sequence 27987, A
16	55	14.2	547	7	US-11-953-697-2751	Sequence 2751, Ap
17	54	14.0	456	7	US-11-106-014-12	Sequence 12, Appl
18	53.5	13.9	338	7	US-10-953-349-38513	Sequence 38513, A
19	53.5	13.9	365	7	US-10-511-937-2530	Sequence 2530, Ap
20	53.5	13.9	1058	7	US-11-251-673-3	Sequence 3, Appli
21	53	13.7	193	6	US-10-953-349-9405	Sequence 9405, Ap
22	53	13.7	210	6	US-10-953-349-9404	Sequence 9404, Ap
23	53	13.7	882	6	US-10-196-749-574	Sequence 574, App
24	53	13.7	1038	6	US-10-511-937-2443	Sequence 2443, Ap
25	52.5	13.6	269	6	US-10-511-455-19	Sequence 19, Appl
26	52.5	13.6	308	6	US-10-511-455-23	Sequence 23, App
27	52.5	13.6	308	6	US-10-511-455-25	Sequence 25, Appl
28	52.5	13.6	314	6	US-10-511-455-21	Sequence 21, Appl
29	52.5	13.6	347	6	US-10-511-455-17	Sequence 17, Appl
30	52.5	13.6	347	6	US-10-511-455-28	Sequence 28, Appl
31	52.5	13.6	348	6	US-10-505-928-399	Sequence 399, App
32	52.5	13.6	348	6	US-10-511-455-15	Sequence 15, Appl
33	52.5	13.6	348	6	US-10-511-455-27	Sequence 27, Appl
34	52.5	13.6	350	6	US-10-511-455-29	Sequence 29, Appl
35	52.5	13.6	410	6	US-10-953-349-20599	Sequence 20599, A
36	52.5	13.6	430	6	US-10-953-349-20598	Sequence 20598, A
37	52.5	13.6	451	7	US-10-953-349-20597	Sequence 20597, A
38	52.5	13.6	791	7	US-11-318-939-6	Sequence 6, Appli
39	52	13.5	120	6	US-10-953-349-40121	Sequence 40121, A
40	52	13.5	144	6	US-10-953-349-23921	Sequence 23921, A
41	52	13.5	152	6	US-10-953-349-23920	Sequence 23920, A
42	52	13.5	157	6	US-10-953-349-23919	Sequence 23919, A
43	52	13.5	283	6	US-10-953-349-22187	Sequence 22187, A
44	52	13.5	531	6	US-10-953-349-22037	Sequence 22037, A
45	52	13.5	533	6	US-10-953-349-22036	Sequence 22036, A

ALIGNMENTS

RESULT 1
US-11-101-316-30
; Sequence 30, Application US/11101316
; Publication No. US20060099657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; TITLE OF INVENTION: UNDEREXPRESSED IN MELANOMA
; FILE REFERENCE: P2230R1.C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 30
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-101-316-30

Query Match 100.0%; Score 386; DB 7; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.8e-40;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLLTLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60
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Db 1 MLLLTLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60

Qy 61 AQPRGEGEKVGDG 73
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Db 61 AQPRGEGEKVGDG 73

RESULT 2

US-10-953-349-14153
; Sequence 14153, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 14153
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Glycine max

Qy US-10-953-349-14153
Db US-10-953-349-14153

Query Match   16.3%; Score 63; DB 6; Length 124;
Best Local Similarity   28.0%;
Matches   26; Conservative   11; Mismatches   32; Indels   24; Gaps   4;

Qy   2 LLLTLLLL|--------------LLLKGSC------------LEWGLVGAQKVSSATDAPIRDW 39
         : |||||||| ||||||:||||||
Db   9 ILLTLSLLVRHEKRFSCFFFFFVVNVSCEFDDKTNVKAAWGKVGAHAGEYGAEALERMF 68

Qy 40 AFFPPSFLCLLPHRPAMTCSQAQPRGEGEKVGD 72
        :||:||||:   :||:
Db 69 LSFPTT-KTYPHFD-LSHGSAQVKGHGKKVAD 99

RESULT 3
US-10-953-349-30624
; Sequence 30624, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 30624
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Triticum aestivum

Qy US-10-953-349-14153
Db US-10-953-349-30624

Query Match   16.2%; Score 62.5; DB 6; Length 86;
Best Local Similarity   31.9%; Pred. No. 0.38;
Matches   23; Conservative   3; Mismatches   29; Indels   17; Gaps   3;

Qy 16 SCLEWGLVGAQKVSSATDAPIRDW---AFF-----PPSFLCLLPHRPAM------TC 58
        |: | || | :|| |||||||:|||| ||
Db 15 SCSSTSPAGLQAPASAGRLPPAAWCPPAVEGSPSARPPAAPCGGARRPQQGNSLGHGNGC 74

Qy 59 SQAQPRGEGEKV 70
          :||||||:|
Db 75 GGASPAGEGEEV 86

RESULT 4
US-10-953-349-14154
; Sequence 14154, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 14154
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Glycine max

Qy US-10-953-349-14154
Db US-10-953-349-14154

Query Match   15.3%; Score 59; DB 6; Length 91;
Best Local Similarity   34.0%; Pred. No. 1.1;
Matches   18; Conservative   7; Mismatches   26; Indels   2; Gaps   2;

Qy 20 WGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQPRGEGEKVGD 72
        ||:||| | ::|:| ::| |||||:||||:   :||:
Db 16 WGKVGAHAGEYGAEALERMFLSFPTT-KTYPHFD-LSHGSAQVKGHGKKVAD 66

RESULT 5
US-10-511-937-2432
; Sequence 2432, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50661200104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2432
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-511-937-2432

Qy US-10-953-349-14154
Db US-10-511-937-2432

Query Match   15.3%; Score 59; DB 6; Length 142;
Best Local Similarity   34.0%; Pred. No. 1.7;
Matches   18; Conservative   7; Mismatches   26; Indels   2; Gaps   2;

Qy 20 WGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQPRGEGEKVGD 72
        ||:||| | ::|:| ::| |||||:||||:   :||:
Db 16 WGKVGAHAGEYGAEALERMFLSFPTT-KTYPHFD-LSHGSAQVKGHGKKVAD 65

RESULT 6
US-10-953-349-10909
; Sequence 10909, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 10909

RESULT 7

; SEQ ID NO 10908
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10908

; US-10-953-349-10908
; Sequence 10908, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3

Query Match   15.3%; Score 59; DB 6; Length 468;
Best Local Similarity 34.0%; Pred. No. 6.1;
Matches 18; Conservative 7; Mismatches 26; Indels 2; Gaps 2;

Qy   20 WGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQPREGEGEKVGD 72
Db 393 WGKVGAHAGEYGAEALERMFLSFPTT-KTYFPHFD-LSHGSAQVKGHGKKVAD 443

RESULT 8

; SEQ ID NO 10907
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10907

; US-10-953-349-10907
; Sequence 10907, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3

Query Match   15.3%; Score 59; DB 6; Length 469;
Best Local Similarity 34.0%; Pred. No. 6.1;
Matches 18; Conservative 7; Mismatches 26; Indels 2; Gaps 2;

Qy   20 WGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQPRGEGEKVGD 72
Db 394 WGKVGAHAGEYGAEALERMFLSFPTT-KTYFPHFD-LSHGSAQVKGHGKKVAD 444

RESULT 9

; US-10-953-349-35222
; Sequence 35222, Application US/10953349

Query Match   15.3%; Score 59; DB 6; Length 503;
Best Local Similarity 34.0%; Pred. No. 6.6;
Matches 18; Conservative 7; Mismatches 26; Indels 2; Gaps 2;

Qy   20 WGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQPREGEGEKVGD 72
Db 428 WGKVGAHAGEYGAEALERMFLSFPTT-KTYFPHFD-LSHGSAQVKGHGKKVAD 478

; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 35222
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (48)..(48)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (81)..(81)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-35222

Query Match   15.3%; Score 58.5; DB 6; Length 155;
Best Local Similarity 35.0%; Pred. No. 2.2;
Matches 14; Conservative 5; Mismatches 16; Indels 5; Gaps 2;

Qy   30 SATDAPIRDWAFFP-----PSFLCLLP-HRPAMTCSQAPQR 64
Db 103 SPSSSPTRSWVFWPAGTCSAFCCSLRLEGSAMACPSSTPR 142

RESULT 10

; US-10-196-749-74
; Sequence 74, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P34301C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28

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;  PRIOR FILING DATE: 1997-10-28
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
;  SEQ ID NO 74
;  TYPE: PRT
;  LENGTH: 432
;  ORGANISM: Homo Sapien
US-10-196-749-74

Qy  Query Match      15.0%;  Score 58;  DB 6;  Length 432;
    Best Local Similarity   43.8%;
    Matches  14;  Conservative  3;  Pred. No. 7,4;  Mismatches  15;  Indels  0;  Gaps  0;

Qy  4   LTLLLLLLLKGSCLEWGLVGAQKVSSATDAP  35
            |||||||||||    ||    ||:| ::||
Db  18  LTALLLLLLGHGGGGRWGARAQEAAAAAADGP  49
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RESULT 11
US-10-953-349-35817

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;  Sequence 35817, Application US/10953349
;  Publication No. US20060107345A1
;  GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE: 2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: Patentin version 3.3
;  SEQ ID NO 35817
;  LENGTH: 166
;  TYPE: PRT
;  ORGANISM: Zea mays subsp. mays
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (11)..(11)
;  OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (137)..(137)
;  OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-35817

Qy  Query Match      14.9%;  Score 57.5;  DB 6;  Length 166;
    Best Local Similarity   28.1%;
    Matches  27;  Conservative  6;  Pred. No. 3,1;  Mismatches  24;  Indels  39;  Gaps  5;

Qy  4   LTLLLLLLLKGSCLEWGLVG-----------AQKVSSATDAPI-------------------RDW  39
            ||||||||||||          ::  ::||:||||||
Db  22  LTLLLPLLLASPSLPSAAAAPSPPTVPATORQAASASDAPSPPPPPPAQQHPRRHRHRHW  81

Qy  40  AFFPPSFLCLLPHRPAMTCSQAQPRGE----GEKVG  71
            ||||  ||||         |:::|
Db  82  KHRPPP-----PHPP------PPPRRRLNFGERLG  106
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RESULT 12
US-10-953-349-35815

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;  Sequence 35815, Application US/10953349
;  Publication No. US20060107345A1
;  GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE: 2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: Patentin version 3.3
;  SEQ ID NO 35815
;  LENGTH: 215
;  TYPE: PRT
;  ORGANISM: Zea mays subsp. mays
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (60)..(60)
;  OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (186)..(186)
;  OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-35815

Qy  Query Match      14.9%;  Score 57.5;  DB 6;  Length 215;
    Best Local Similarity   28.1%;
    Matches  27;  Conservative  6;  Pred. No. 4,1;  Mismatches  24;  Indels  39;  Gaps  5;

Qy  4   LTLLLLLLLKGSCLEWGLVG-----------AQKVSSATDAPI-------------------RDW  39
            ||||||||||||          ::  ::||:||||||
Db  71  LTLLLPLLLASPSLPSAAAAPSPPTVPATORQAASASDAPSPPPPPPAQQHPRRHRHRHW  130

Qy  40  AFFPPSFLCLLPHRPAMTCSQAQPRGE----GEKVG  71
            ||||  ||||         |:::|
Db  131  KHRPPP-----PHPP------PPPRRRLNFGERLG  155
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RESULT 13
US-10-953-349-15677

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;  Sequence 15677, Application US/10953349
;  Publication No. US20060107345A1
;  GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE: 2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: Patentin version 3.3
;  SEQ ID NO 15677
;  LENGTH: 208
;  TYPE: PRT
;  ORGANISM: Glycine max
US-10-953-349-15677

Qy  Query Match      14.5%;  Score 56;  DB 6;  Length 208;
    Best Local Similarity   56.5%;
    Matches  13;  Conservative  4;  Pred. No. 6;  Mismatches  6;  Indels  0;  Gaps  0;

Qy  1   MLLLTLLLLLLLKGSCLEWGLV  23
           |||| || ||||||||
Db  85  LLLLLLLLQLLLLLRPLLLQWQLL  107
```

RESULT 14
US-11-312-797-2

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;  Sequence 2, Application US/11312797
;  Publication No. US20060100151A1
;  GENERAL INFORMATION:
;  APPLICANT: Trout, Anthony
;  TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
;  NUMBER OF SEQUENCES: 4
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Immunex Corporation
;  STREET: 51 University Street
;  CITY: Seattle
;  STATE: WA
;  COUNTRY: USA
;  ZIP: 98101
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: Apple PowerMacintosh
;  OPERATING SYSTEM: Apple Operating System 7.5.5
;  SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
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;   CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/11/312,797
;      FILING DATE: 20-Dec-2005
;      CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US/08/978,773
;      FILING DATE: 26-Nov-1997
;      APPLICATION NUMBER: USSN 60/052,525
;      FILING DATE: 27 NOVEMBER 1996
;   ATTORNEY/AGENT INFORMATION:
;      NAME: Perkins, Patricia Anne
;      REGISTRATION NUMBER: 34,693
;      REFERENCE/DOCKET NUMBER: 2623-A
;   TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (206)587-0430
;      TELEFAX: (206)
;   INFORMATION FOR SEQ ID NO: 2:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 864 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-11-312-797-2

Query Match             14.5%;  Score 56;  DB 7;  Length 864;
Best Local Similarity   32.8%;  Pred. No. 27;
Matches    19;  Conservative    8;  Mismatches   21;  Indels  10;  Gaps   3;

Qy          3 LLTLLLLLLLLLKGS------------CLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRP 54
              |:||:|       |:||          |:||||:| |:||| |:.::|.|||: ||||||:|||
Db        326 LITLIAILLV--GSVIVLIICMTWRLSGADQEKHGDDSKIN--GILPVADLTPPLRP 379


RESULT 15
US-10-953-349-27987
;  Sequence 27987, Application US/10953349
;  Publication No. US20060107345A1
;  GENERAL INFORMATION:
;     APPLICANT: ALEXANDROV, Nickolai et al.
;     TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;     TITLE OF INVENTION: ENCODED THERBY
;     FILE REFERENCE: 2750-1579PUS2
;     CURRENT APPLICATION NUMBER: US/10/953,349
;     CURRENT FILING DATE: 2004-09-30
;     NUMBER OF SEQ ID NOS: 40252
;     SOFTWARE: PatentIn version 3.3
;  SEQ ID NO 27987
;     LENGTH: 85
;     TYPE: PRT
;     ORGANISM: Triticum aestivum
US-10-953-349-27987

Query Match             14.2%;  Score 55;  DB 6;  Length 85;
Best Local Similarity   35.6%;  Pred. No. 3.1;
Matches    21;  Conservative    3;  Mismatches   25;  Indels  10;  Gaps   2;

Qy         25 AQKVSSATDA-----PIRDWAFFP------PSFLCLLPHRPAMTCSQAQPRGEGEKVGDG 73
              |:| |::..     |:||| ||          |||| |
Db         17 AQRQRSAASGHGLLPGVRDAAADPAGHRRPPPAPLLPHLPVRLPHQKQDREEGEASGOEG 75
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Search completed: June 6, 2006, 21:54:32
Job time : 17 secs

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OM protein - protein search, using sw model

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GenCore version 5.1.9

Run on: June 9, 2006, 00:30:31 ; Search time 185 Seconds (without alignments) 182.782 Million cell updates/sec

Perfect score: 386
Sequence: 1 MLLILTLLLLLLLLKGSCLEW..........PAMTCSQAQPRGEGEKVGDG 73

Scoring table: BLOSUM62
Searched: Gapop 10.0 , Gapext 0.5
Searched: 2097797 seqs, 46321485B residues

Total number of hits satisfying chosen parameters: 2097797
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 1500 summaries

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Published Applications AA Main:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
93	386	100.0	73	4	US-10-063-742-30	Sequence 30, Appl
168	386	100.0	73	4	US-10-013-909A-22	Sequence 22, Appl
215	386	100.0	73	4	US-10-972-317-30	Sequence 30, Appl
217	386	100.0	73	6	US-10-025-607-22	Sequence 22, Appl
218	386	100.0	73	6	US-11-102-240-30	Sequence 30, Appl
219	386	100.0	73	6	US-11-103-195-30	Sequence 30, Appl
220	72	18.7	892	4	US-11-437-963-197731	Sequence 197731,
221	70.5	18.3	230	5	US-10-821-273-40	Sequence 40, Appli
222	70.5	18.3	506	4	US-10-734-049A-270	Sequence 270, App
223	69.5	18.0	225	4	US-10-243-552-601	Sequence 601, Appl
224	68	17.6	930	3	US-10-918-171A-2	Sequence 2, Appli
225	67.5	17.5	669	3	US-09-983-204-15	Sequence 15, Appl
226	67.5	17.5	669	4	US-10-097-340-278	Sequence 278, App
227	67.5	17.5	669	4	US-10-097-340-280	Sequence 280, App
228	67.5	17.5	669	4	US-10-373-801-28	Sequence 28, Appl
229	67.5	17.5	669	4	US-10-133-573-4	Sequence 4, Appli
230	67.5	17.5	669	5	US-10-741-601-466	Sequence 466, Appl
231	67.5	17.5	669	5	US-10-741-600-1350	Sequence 1350, App
232	67.5	17.5	669	5	US-10-887-233-4	Sequence 4, Appli
233	67.5	17.5	669	6	US-11-050-926-278	Sequence 278, App
234	67.5	17.5	669	6	US-11-050-926-280	Sequence 280, App
235	67.5	17.5	158	4	US-10-767-701-56878	Sequence 56878, A
236	67	17.4	535	5	US-10-723-860-4109	Sequence 4109, Ap
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334	59.5	15.4	59	3	US-10-621-401-261	Sequence 261, App
335	59.5	15.4	59	3	US-09-305-736-261	Sequence 261, App
336	59.5	15.4	59	4	US-10-818-683-261	Sequence 261, App
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1170	57	14.8	392	5	US-10-425-115-304480	Sequence 304480,
1171	57	14.8	435	6	US-10-467-657-5724	Sequence 5724, Ap
1172	57	14.8	487	5	US-10-437-963-142254	Sequence 142254,
1173	57	14.8	602	3	US-10-148-641A-12	Sequence 12, Appli
1174	57	14.8	681	6	US-09-908-193-4	Sequence 4, Appli
1175	57	14.8	709	5	US-11-188-298-17684	Sequence 17684, A
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1179	57	14.8	908	4	US-11-097-143-7659	Sequence 7659, Ap
1180	57	14.8	3298	4	US-11-097-143-7593	Sequence 7593, Ap
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1182	57	14.8	3298	4	US-10-160-758-16	Sequence 16, Appl
1183	57	14.8	3298	4	US-10-174-677-8	Sequence 8, Appli
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1185	56.5	14.6	2448	4	US-10-210-172-50	Sequence 50, Appl
1186	56.5	14.6	3298	4	US-10-425-115-306113	Sequence 306113,
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1403	56.5	14.6	151	4	US-10-223-085-212	Sequence 212, App
1404	56.5	14.6	151	4	US-10-223-084-212	Sequence 212, App
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1406	56.5	14.6	151	4	US-10-223-090-212	Sequence 212, App
1408	56.5	14.6	151	4	US-10-223-087-212	Sequence 212, App
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Job time : 208 secs

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OM protein - protein search, using sw model

Copyright (c) 1993 - 2006 Biocceleration Ltd.
GenCore version 5.1.9

Run on: June 6, 2006, 21:38:54 ; Search time 51 Seconds

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Perfect score: 386
Sequence: 1 MLLTLLLLLLKGSCLEW.............PAMTCSQAPRGEGEKVGDG 73

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Gapop 10.0 , Gapext 0.5
Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	386	100.0	73	2	US-10-012-231A-22	Sequence 22, Appl
2	386	100.0	73	2	US-10-015-389A-22	Sequence 22, Appl
3	386	100.0	73	2	US-10-006-768A-22	Sequence 22, Appl
4	386	100.0	73	2	US-10-015-671A-22	Sequence 22, Appl
5	386	100.0	73	2	US-10-015-393A-22	Sequence 22, Appl
6	386	100.0	73	2	US-10-011-833A-22	Sequence 22, Appl
7	386	100.0	73	2	US-10-006-041A-22	Sequence 22, Appl
8	386	100.0	73	2	US-10-012-064A-22	Sequence 22, Appl
9	386	100.0	73	2	US-10-015-392A-22	Sequence 22, Appl
10	386	100.0	73	2	US-10-011-795B-22	Sequence 22, Appl
11	386	100.0	73	2	US-10-015-386A-22	Sequence 22, Appl
12	386	100.0	73	2	US-10-012-121A-22	Sequence 22, Appl
13	386	100.0	73	2	US-10-006-485A-22	Sequence 22, Appl
14	386	100.0	73	2	US-10-006-746A-22	Sequence 22, Appl
15	386	100.0	73	2	US-10-012-752A-22	Sequence 22, Appl
16	386	100.0	73	2	US-10-012-253A-22	Sequence 22, Appl
17	386	100.0	73	3	US-10-017-253A-22	Sequence 22, Appl
18	386	100.0	73	3	US-10-015-519A-22	Sequence 22, Appl
19	386	100.0	73	3	US-10-015-715A-22	Sequence 22, Appl
20	386	100.0	73	3	US-10-007-235A-22	Sequence 22, Appl
21	72	19.9	312	2	US-09-270-767-44974	Sequence 44974, A
22	72	18.7	884	1	US-08-465-976A-2	Sequence 2, Appli
23	72	18.7	884	1	US-08-982-412-2	Sequence 2, Appli
24	68	17.6	930	2	US-09-369-364A-2	Sequence 2, Appli
25	67.5	17.5	702	2	US-09-917-254-94	Sequence 94, Appl
26	62.5	16.2	270	1	US-08-978-404B-8	Sequence 8, Appli
27	62.5	16.2	307	2	US-09-252-991A-32304	Sequence 32304, A
28	62	16.1	484	2	US-09-248-796A-17959	Sequence 17959, A
29	62	16.1	896	2	US-09-585-858-17	Sequence 17, Appl
30	62	16.1	896	2	US-10-270-878-17	Sequence 17, Appl
31	62	16.1	1238	2	US-09-900-065-2	Sequence 2, Appli
32	62	16.1	1238	2	US-09-904-065-14	Sequence 14, Appl
33	62	16.1	1240	1	US-08-680-326-37	Sequence 37, Appli
34	62	16.1	1240	2	US-09-904-065-4	Sequence 4, Appli
35	62	16.1	1240	2	US-09-904-065-15	Sequence 15, Appli
36	61	15.9	578	2	US-09-503-172A-2	Sequence 2, Appli
37	61	15.8	152	2	US-09-800-729-84	Sequence 84, Appli
38	60.5	15.7	136	2	US-10-094-749-2654	Sequence 2654, Ap
39	60.5	15.7	274	1	US-08-484-905-105	Sequence 105, Appl
40	60.5	15.7	274	1	US-08-484-905-107	Sequence 107, Appl
41	60.5	15.7	274	1	US-08-484-905-108	Sequence 108, Appl
42	60.5	15.7	274	2	US-08-481-985B-105	Sequence 105, Appl
43	60.5	15.7	274	2	US-08-481-985B-107	Sequence 107, Appl
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ALIGNMENTS

RESULT 1
US-10-012-231A-22

; Sequence 22, Application US/10012231A
; Patent No. 6924355
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C23
; CURRENT APPLICATION NUMBER: US/10/012,231A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/10/012,231A
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-012-231A-22

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Best Local Similarity   100.0%;
Matches   73; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   61 AQPRGEGEKVGDG 73

Db   61 AQPRGEGEKVGDG 73
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RESULT 2
US-10-015-389A-22
; Sequence 22, Application US/10015389A
; Patent No. 6936436
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C48
; CURRENT APPLICATION NUMBER: US/10/015,389A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-015-389A-22

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Qy   61 AQPRGEGEKVGDG 73
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; Sequence 22, Application US/10006768A
; Patent No. 6936697
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.

; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-015-671A-22

  Query Match   100.0%; Score 386; DB 2; Length 73;
  Best Local Similarity 100.0%; Pred. No. 1.4e-43;
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Qy   61 AQPRGEGEKVGDG 73
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Db   61 AQPRGEGEKVGDG 73
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RESULT 5
US-10-015-393A-22
; Sequence 22, Application US/10015393A
; Patent No. 6951737
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C46
; CURRENT APPLICATION NUMBER: US/10,015,393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; FEATURE:
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-015-393A-22

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Qy   61 AQPRGEGEKVGDG 73
Db   61 AQPRGEGEKVGDG 73
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; Sequence 22, Application US/10011833A

; Patent No. 6951920
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C22
; CURRENT APPLICATION NUMBER: US/10/011,833A
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; NUMBER OF SEQ ID NOS: 477
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; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; FEATURE:
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
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; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-011-833A-22

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RESULT 7
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; Sequence 22, Application US/10006041A
; Patent No. 6951921
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C8
; CURRENT APPLICATION NUMBER: US/10/006,041A

; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-006-041A-22

Query Match   100.0%; Score 386; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.4e-43;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   61 AQPRGEGEKVGDG 73
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Db   61 AQPRGEGEKVGDG 73

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US-10-012-064A-22
Sequence 22, Application US/10012064A
; Patent No. 6953841
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C19
; CURRENT APPLICATION NUMBER: US/10/012,064A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
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; PRIOR FILING DATE: 1998-09-09

; PRIOR FILING DATE: 1998-09-09
; Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-012-064A-22

Query Match   100.0%; Score 386; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.4e-43;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60
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Db   1 MLLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60

Qy   61 AQPRGEGEKVGDG 73
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Db   61 AQPRGEGEKVGDG 73

RESULT 9
US-10-015-392A-22
Sequence 22, Application US/10015392A
; Patent No. 6972186
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C58
; CURRENT APPLICATION NUMBER: US/10/015,392A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09

RESULT 10
US-10-011-795B-22
Sequence 22, Application US/10011795B
Patent No. 7012131
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan 1.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C25
CURRENT APPLICATION NUMBER: US/10/011,795B
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
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PRIOR FILING DATE: 1998-09-01
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PRIOR APPLICATION NUMBER: 60/098536
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 22
  LENGTH: 73
  TYPE: PRT
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: sig_peptide
  LOCATION: 1-15
  OTHER INFORMATION: Signal peptide.
  FEATURE:
  NAME/KEY: misc_feature
  LOCATION: 3-18
  OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-011-795B-22

Query Match   100.0%; Score 386; DB 2; Length 73;
Best Local Similarity   100.0%; Pred. No. 1.4e-43;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   1 MLLLTLLLLLLLLLLKGSCLEWGLVGAQKVSSAATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60

Qy   61 AQPRGEGEKVGDG 73
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Db   61 AQPRGEGEKVGDG 73

RESULT 11
US-10-015-386A-22
Sequence 22, Application US/10015386A
Patent No. 7022498
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan 1.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C55
CURRENT APPLICATION NUMBER: US/10/015,386A
CURRENT FILING DATE: 2001-12-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 22
  LENGTH: 73
  TYPE: PRT
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: sig_peptide
  LOCATION: 1-15
  OTHER INFORMATION: Signal peptide.
  FEATURE:
  NAME/KEY: misc_feature
  LOCATION: 3-18
  OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-015-386A-22

Query Match   100.0%; Score 386; DB 3; Length 73;
Best Local Similarity   100.0%; Pred. No. 1.4e-43;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   1 MLLLTLLLLLLLLLLKGSCLEWGLVGAQKVSSAATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60

Qy   61 AQPRGEGEKVGDG 73
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Db   61 AQPRGEGEKVGDG 73

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Db    1  MLLITLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ  60

Qy   61  AQPRGEGEKVGDG  73
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Db   61  AQPRGEGEKVGDG  73
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RESULT 12
US-10-012-121A-22
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; Patent No. 7022817
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C20
; CURRENT APPLICATION NUMBER: US/10/012,121A
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-012-121A-22

  Query Match   100.0%; Score 386; DB 3; Length 73;
  Best Local Similarity   100.0%; Pred. No. 1.4e-43;
  Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db    1  MLLITLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ  60

Qy   61  AQPRGEGEKVGDG  73
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Db   61  AQPRGEGEKVGDG  73
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RESULT 13
US-10-006-485A-22
; Sequence 22, Application US/10006485A
; Patent No. 7026448
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C9
; CURRENT APPLICATION NUMBER: US/10/006,485A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
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; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684

RESULT 14
US-10-006-746A-22
Sequence 22, Application US/10006746A
Patent No. 7026449
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan 1.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey

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Query Match       100.0%;  Score 386;  DB 3;  Length 73;
Best Local Similarity   100.0%;  Pred. No. 1.4e-43;
Matches   73;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    1  MLLTLTLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ   60

Qy   61  AQPRGEGEKVGDG   73
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Db   61  AQPRGEGEKVGDG   73
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PRIOR APPLICATION NUMBER: 60/103395
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103328
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103315

PRIOR FILING DATE: 1998-09-17
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PRIOR APPLICATION NUMBER: 60/103258
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103314
PRIOR FILING DATE: 1998-10-07

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C5
CURRENT APPLICATION NUMBER: US/10/006,746A
CURRENT FILING DATE: 2001-12-06

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; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

RESULT 15
US-10-012-752A-22
; Sequence 22, Application US/10012752A
; Patent No. 7026455
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C24
; CURRENT APPLICATION NUMBER: US/10/012,752A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US/10/012,752A
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-012-752A-22

Query Match   100.0%; Score 386; DB 3; Length 73;
Best Local Similarity   100.0%; Pred. No. 1.4e-43;
Matches 73; Conservative   0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPPSFLCLLPHRPAMTCSQ 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPPSFLCLLPHRPAMTCSQ 60

Qy   61 AQPRGEGEKVGDG 73
            |||||||||||||
Db   61 AQPRGEGEKVGDG 73

Search completed: June 6, 2006, 21:40:16
Job time : 52 secs

Query Match   100.0%; Score 386; DB 3; Length 73;
Best Local Similarity   100.0%; Pred. No. 1.4e-43;
Matches 73; Conservative   0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPPSFLCLLPHRPAMTCSQ 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPPSFLCLLPHRPAMTCSQ 60

Qy   61 AQPRGEGEKVGDG 73
            |||||||||||||
Db   61 AQPRGEGEKVGDG 73

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OM protein - protein search, using sw model

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GenCore version 5.1.9

Run on: June 6, 2006, 21:30:19 ; Search time 294 Seconds
                                          (without alignments)
                                          229.681 Million cell updates/sec

Post-processing: Minimum Match 0%
Maximum DB seq length: 200000000
Minimum DB seq length: 0

Title: US-10-063-534-30
Perfect score: 386
Sequence: 1 MLLLTLLLLLLLKGSCLEW..........PAMTCSQAQPRGEGEKVGDG 73

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Maximum Match seq length: 200000000
Minimum Match 0%

Database :   UniProt_7.2:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*
                 Listing first 45 summaries
                 Maximum Match 100%

Scoring table: Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result   %   Query
No.   Score   Match Length DB ID   Description
------- -----   ----- ------ -- --   -----------

  1   386   100.0   73   2 Q6UWT3_HUMAN   homo sapien
  2   85   22.0   144   2 Q4S4J9_TETNG   tetraodon n
  3   77   19.9   116   2 Q8T3M4_DROME   drosophila
  4   77   19.9   125   2 Q8IR67_DROME   drosophila
  5   75.5   19.6   468   2 Q4V7Z1_XENLA   xenopus lae
  6   73.5   19.0   379   2 Q6DIJ0_XENTR   xenopus tro
  7   72   18.7   892   2 Q53P51_ORYSA   oryza sativ
  8   71.5   18.5 1912   2 Q53P51_ORYSA   oryza sativ
  9   71   18.4   878   2 Q4D8X5_TRYCR   trypanosoma
 10   70.5   18.3   506   2 CK5P3_HUMAN   homo sapien
 11   70.5   18.3   506   2 CK5P3_PONPY   pongo pygma
 12   70   18.1   257   1 DCH_THAAR   thauera aro
 13   69.5   18.0   130   2 Q6IGC8_DROME   drosophila
 14   69   17.9   462   2 KREM2_HUMAN   homo sapien
 15   69   17.9   652   2 Q4RTS7_TETNG   tetraodon n
 16   68   17.6   307   2 Q7S7R5_NEUCR   neurospora
 17   68   17.6   725   2 Q8CB87_MOUSE   mus musculu
 18   68   17.6   930   1 ATS5_MOUSE   mus musculu
 19   67.5   17.5   669   1 SCNAA_HUMAN   homo sapien
 20   67.5   17.5   669   2 Q6GSQ6_HUMAN   homo sapien
 21   67.5   17.5 3898   2 Q2UAI4_ASPOR   aspergillus
 22   67.5   17.5 5255   2 Q2PC93_CHICK   gallus gall
 23   67   17.4   159   2 Q7PLY2_ANOGA   anopheles g
 24   67   17.4   159   2 Q8I8T2_ANOGA   anopheles g
 25   67   17.4   351   2 Q72AN6_DESVH   desulfovibr
 26   66.5   17.4   535   2 Q15175_HUMAN   homo sapien
 27   66.5   17.2   557   2 Q6G5M3_BARHE   bartonella
 28   66   17.1   71   2 Q9R1E7_MOUSE   mus musculu
 29   66   17.1   557   2 Q9R1E7_MOUSE   mus musculu
 30   66   17.1   368   2 Q89R59_BRAJA   bradyrhizob
 31   66   17.1   385   2 Q31IK8_THICR   thiomicrosp
 32   65.5   17.0   73   2 Q3K6Z7_PSEPF   pseudomonas
 33   65.5   17.0   223   2 Q31SY9_DESDG   desulfovibr
 34   65.5   17.0   157   2 Q922X9_RAT   rattus norv
 35   65   16.8   157   2 Q876R9_ANOGA   anopheles g
 36   65   16.8 1327   2 Q2P0Z1_XANOR   xanthomonas
 37   64.5   16.7   207   2 Q5JN21_ORYSA   oryza sativ
 38   64.5   16.7   407   2 Q7VW14_BORPE   bordetella
 39   64.5   16.7   407   2 Q7W553_BORPA   bordetella
 40   64.5   16.7   407   2 Q7WCN5_BORBR   bordetella
 41   64   16.6   103   2 Q7U7R9_SYNPX   synechococc
 42   64   16.6   164   2 Q5TSA0_HUMAN   homo sapien
 43   64   16.6   210   2 Q6I177_DROME   drosophila
 44   64   16.6   862   2 Q4PCZ1_USTMA   ustilago ma
 45   64   16.6 1029   2 Q7S2D9_NEUCR   neurospora

ALIGNMENTS

RESULT 1
Q6UWT3_HUMAN
ID   Q6UWT3_HUMAN   PRELIMINARY;   PRT;   73 AA.
AC   Q6UWT3;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   APELIN.
OR   ORFNames=UNQ471;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Wu M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
CC   ---
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---
DR   EMBL; AY358657; AAQ89020.1; -; mRNA.
SQ   SEQUENCE   73 AA; 7879 MW; A99C96797BCC4D91 CRC64;

Query Match   100.0%;   Score 386; DB 2; Length 73;
Best Local Similarity   100.0%;
Matches   73; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFPPPSFICLLPHRPAMTCSQ   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFPPPSFICLLPHRPAMTCSQ   60

Qy   61 AQPRGEGEKVGDG   73
             |||||||||||||
Db   61 AQPRGEGEKVGDG   73

RESULT 2
Q4S4J9_TETNG
ID   Q4S4J9_TETNG   PRELIMINARY;   PRT;   144 AA.
AC   Q4S4J9;

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DT   19-JUL-2005, integrated into UniProt/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
GN   ORFNames=GSTENG00024149001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Euteleostei; Percomorpha; Tetraodontiformes;
OC   Tetraodontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15496914; DOI=10.1038/nature03025;
RA   Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
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DR   EMBL; CAAE01014738; CAG04433.1; -; Genomic_DNA.
FT   NON_TER          144
SQ   SEQUENCE   144 AA;  15706 MW;  420C361E79054I9D CRC64;

Query Match             22.0%;  Score 85;  DB 2;  Length 144;
Best Local Similarity   38.6%;  Pred. No. 0.12;
Matches   27;  Conservative   8;  Mismatches  29;  Indels   6;  Gaps   2;

Qy          1  MLLLTLTLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQ 60
               :||||||||||||:|||||||||||||||||||||||:|||||:||||.|||.|
Db          6  VVLLPLSLVLLLGGIC--GLVSSLAQSRALLTATASPFFICKTFCCFLPKKCSFTLS- 61

Qy         61  AQPRGEGEKV 70
               :|||||:|||
Db         62  --PRTEGVAV 69


RESULT 3
Q8T3M4_DROME
ID   Q8T3M4_DROME    PRELIMINARY;    PRT;   116 AA.
AC   Q8T3M4;
DT   01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2002, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   ORFNames=CG32534; (Fragment).
GN   GM08788p (Fragment).
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.


RESULT 4
Q8IR67_DROME
ID   Q8IR67_DROME    PRELIMINARY;    PRT;   125 AA.
AC   Q8IR67;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   ORFNames=CG32634, Dmel_CG32634;
GN   ORFNames=CG32634;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
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```
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA   George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA   Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paglej V., Park S.,
RA   Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA   Celniker S.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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DR   EMBL; AY094760; AAM11113.1; -; mRNA.
DR   FlyBase; FBgn0052634; CG32634.
SQ   SEQUENCE   116 AA;  12750 MW;  94A6D36789A712BD CRC64;

Query Match             19.9%;  Score 77;  DB 2;  Length 116;
Best Local Similarity   37.3%;  Pred. No. 0.83;
Matches   19;  Conservative   9;  Mismatches  19;  Indels   4;  Gaps   1;

Qy          1  MLLLTLTLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLP 51
               ||| |||||||||||:
Db         64  LLLLLLLLLLLLQ---QEHLAASQQIDLEAEKPLVDFLLVPPLSSCTFP 110


RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Murzin D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
```

RESULT 5

ID   Q4VZ21_XENLA   PRELIMINARY;   PRT;   468 AA.

RA   Wang Z.-Y., Wassarman D.A., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RG   Berkeley Drosophila Genome Project;
RA   Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA   Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA   Yu C., Rubin G.;
RT   "Drosophila melanogaster release 4 sequence.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RG   FlyBase;
RL   Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.

DR   EMBL; AE003492; AAN09329.1; -; Genomic_DNA.
DR   FlyBase; FBgn0052634; CG32634.
SQ   SEQUENCE 125 AA; 13934 MW; 33654FFB0C2852C9 CRC64;

Query Match   19.9%; Score 77; DB 2; Length 125;
Best Local Similarity   37.3%;
Matches 19; Conservative   9; Mismatches 19; Indels   4; Gaps   1;

Qy   1 MLLLTLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLP 51
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Db   73 LLLLLLLLLLLLQ---QEHLAASQQIDLEAEKPLVDFLLVPPLSSCTFP 119

AC   Q4VZ21;
DT   05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Hypothetical protein.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Ovary;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Ovary;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Ovary;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.

DR   EMBL; BC097649; AAH97649.1; -; mRNA.
DR   InterPro; IPR001680; WD40.
DR   Pfam; PF00400; WD40; 7.
DR   PRINTS; PR00320; GPROTEINBRPT.
DR   ProDom; PD000018; WD40; 7.
DR   SMART; SM00320; WD40; 7.
DR   PROSITE; PS00678; WD_REPEATS_1; 3.
DR   PROSITE; PS00082; WD_REPEATS_2; 7.
DR   PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW   Hypothetical protein; Repeat; WD repeat.
SQ   SEQUENCE 468 AA; 52116 MW; 35C1EB528D2E5564 CRC64;

Query Match   19.6%; Score 75.5; DB 2; Length 468;
Best Local Similarity   35.3%;
Matches 18; Conservative   8; Mismatches 24; Indels   1; Gaps   1;

Qy   16 SCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLP-HRPAMTCSQAQPRG 65
              :|:|: |||:|||:||:||
Db   22 TCVDFSPDSKQLASSSADACVMIWNFKPQSRAYKYPGHKEAVTCVQPSPSG 72

RESULT 6

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Qy
ID   Q6DIJ0_XENTR            PRELIMINARY;      PRT;   379 AA.
AC   Q6DIJ0;
DT   16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT   16-AUG-2004, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   MGC89488 protein.
GN   Name=MGC89488;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
CC   -----------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; BC075548; AAH75548.1; -; mRNA.
DR   Ensembl; ENSXETG00000021865; Xenopus tropicalis.
DR   InterPro; IPR001680; WD40.
DR   Pfam; PF00400; WD40; 7.
DR   PRINTS; PR00320; GPROTEINBRPT.
DR   ProDom; PD000018; WD40; 7.
DR   SMART; SM00320; WD40; 7.
DR   PROSITE; PS00678; WD_REPEATS_1; 3.
DR   PROSITE; PS50082; WD_REPEATS_2; 7.
DR   PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW   Repeat; WD repeat.
SQ   SEQUENCE   379 AA;  42159 MW;  9B576033 7D2D8523 CRC64;

Qy
Best Local Similarity    19.0%;
                         41.9%;          Score  73.5;  DB  2;  Length 379;
Matches   18;   Conservative  4;   Pred. No.  6.7;
                Mismatches  20;   Indels  1;   Gaps  1;

Qy    24 GAQKYSSATDAPIRDWAFFPSFLCLLP-HRPAMTCSQAQPRG  65
Db    30 GKQLASSSADACVMIWNFKPQSRAYKYPGHKEAVTCVQFSPSG 72
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RESULT 7

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ID   Q53P51_ORYSA            PRELIMINARY;      PRT;   892 AA.
AC   Q53P51;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 9.
DT   21-FEB-2006, entry version 1.
DE   Hypothetical protein.
GN   ORFNames=LOC_Os11g08400;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell C., Yuan Q., Ouyang S., Liu J., Wang A., Maiti R., Lin H.,
RA   Zhu W., Hamilton J., Jones K., Tallon L., Feldblyum T., Tsitrin T.,
RA   Bera J., Kim M., Jin S., Padrosh D., Vuong H., Overton II L., Van Aken S.,
RA   Reardon M., Weaver B., Johri S., Lewis M., Utterback T., Iobst S.,
RA   de Vazeilles A., White O., Salzberg S., Fraser C.,
RA   Wortman J., Haas B., Koo H., Zismann V., Hsiao J.,
RA   Buell R.;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell C.R., Wing R.A., McCombie W.A., Ouyang S.;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; AC128644; AAX96348.1; -; Genomic_DNA.
DR   EMBL; DP000010; ABA91822.1; -; Genomic_DNA.
DR   InterPro; IPR001680; WD40.
DR   Pfam; PF00400; WD40; 6.
DR   PRINTS; PR00320; GPROTEINBRPT.
DR   ProDom; PD000018; WD40; 3.
DR   SMART; SM00320; WD40; 5.
DR   PROSITE; PS00678; WD_REPEATS_1; 1.
DR   PROSITE; PS50082; WD_REPEATS_2; 3.
DR   PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW   Hypothetical protein; Repeat; WD repeat.
SQ   SEQUENCE   892 AA;  96390 MW;  D60827E1D111C11 CRC64;

Qy
Best Local Similarity    18.7%;
                         32.0%;          Score  72;  DB  2;  Length 892;
Matches   16;   Conservative  7;   Pred. No.  23;
                Mismatches  27;   Indels  0;   Gaps  0;

Qy    18 LEWGLVGAQKYSSATDAPIRDWAFFPSFLCLLPHRPAMTCSQAQPRGEG  67
Db   538 LAWSMYSQLLLSSSMDKTVRLWDTEAKACLKLFPHNDYVTCVQFNPVDDG 587
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RESULT 8

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ID   Q9ERC1_RAT              PRELIMINARY;      PRT;   1912 AA.
AC   Q9ERC1;
DT   01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2001, sequence version 1.
DT   07-FEB-2006, entry version 19.
DE   Myosin heavy chain Myr 8b.
GN   Name=Loc192253;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=21472394; PubMed=11588169;
RA   Patel K.G., Liu C., Cameron P.L., Cameron R.S.;
RT   "Myr 8, a novel unconventional myosin expressed during brain
```

RT   development associates with the protein phosphatase catalytic subunits
RT   1alpha and 1gamma1.";
RL   J. Neurosci. 21:7954-7968(2001).
RN   [2]
RT   Science 0:0-0(2005).
CC   ---
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---
DR   EMBL; AY004215; AAG23288.1; -; mRNA.
DR   HSSP; P08799; 1MND.
DR   Ensembl; ENSRNOG00000016483; Rattus norvegicus.
DR   RGD; 621561; Loc192253.
DR   GO; GO:0016459; C:myosin; IDA.
DR   GO; GO:0003779; F:actin binding; IDA.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR000048; IQ_CaM_bd_region.
DR   InterPro; IPR001609; Myosin_head.
DR   Pfam; PF00023; Ank; 6.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF00063; Myosin_head; 2.
DR   PRINTS; PR01415; ANKYRIN.
DR   PRINTS; PR00193; MYOSINHEAVY.
DR   ProDom; PD003355; Myosin_head; 1.
DR   SMART; SM00248; ANK; 4.
DR   SMART; SM00242; MYSc; 1.
DR   PROSITE; PS02097; ANK_REP_REGION; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 4.
DR   PROSITE; PS50096; IQ; 1.
SQ   SEQUENCE   1912 AA; 210691 MW; 7C15014A1A83C9C3 CRC64;

Qy   3 LILTLL----LILLLLKGSCLEWGLVGAQKVSSAATDAPIRDWAFFPPSFLCLLPHRPAM- 56
          :| |||| ||:|||||||||||||||||||||||||||||||||:|:| ||||||||:
Db 1457 MLTFLPASPPLFLETRKAIILEAGBGSCQ-------PLKDTCDIPPPFPNLLPHRPPLL 1508

Qy   57 ------TCSQA 61
              ||||||
Db 1509 VFPPTPVTCSPA 1520

Best Local Similarity   18.5%;   Score 71.5;   DB 2;   Length 1912;
Matches   25;   Conservative   4;   Mismatches   22;   Indels   21;   Gaps   3;

Query Match   34.7%;   Pred. No. 55;

RESULT 9
ID   Q4D8X5_TRYCR   PRELIMINARY;   PRT;   878 AA.
AC   Q4D8X5;
DT   13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   13-SEP-2005, sequence version 1.
DT   07-FEB-2006, entry version 2.
DE   Hypothetical protein.
GN   ORFNames=Tc00.1047053506587.20;
OS   Trypanosoma cruzi.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
OC   Schizotrypanum.
OX   NCBI_TaxID=5693;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CL Brener;
RA   El-Sayed N.M.A., Myler P.J., Bartholomeu D.C., Nilsson D.,
RA   Aggarwal G., Tran A.-N., Ghedin E., Worthey E.A., Delcher A.L.,
RA   Blandin G., Westenberger S.J., Caler E., Cerqueira G.C., Branche C.,
RA   Haas B., Anapuma A., Arner E., Aslund L., Attipoe P., Bontempi E.,
RA   Bringaud F., Burton P., Cadag E., Campbell D.A., Carrington M.,
RA   Crabtree J., Darban H., da Silveira J.F., de Jong P., Edwards K.,
RA   Englund P.T., Fazelina G., Feldblyum T., Ferella M., Frasch A.C.,
RA   Gull K., Horn D., Hou L., Huang Y., Kindlund E., Klingbeil M.,
RA   Kluge S., Koo H., Lacerda D., Levin M.J., Lorenzi H., Louie T.,
RA   Machado C.R., McCulloch R., McKenna A., Mizuno Y., Mottram J.C.,
RA   Nelson S., Ochaya S., Osoegawa K., Pai G., Parsons M., Pentony M.,
RA   Pettersson U., Pop M., Ramirez J.L., Rinta J., Robertson L.,
RA   Salzberg S.L., Sanchez D.O., Seyler A., Sharma R., Shetty J.,
RA   Simpson A.J., Sisk E., Tammi M.T., Tarleton R., Teixeira S.,
RA   Van Aken S., Vogt C., Ward P.N., Wickstead B., Wortman J., White O.,

RA   Fraser C.M., Stuart K.D., Andersson B.;
RT   "The Genome Sequence of Trypanosoma cruzi, Etiologic Agent of Chagas'
RT   Disease.";
RL   Science 0:0-0(2005).
RN   [2]
RA   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CL Brener;
RA   El-Sayed N.M.A., Myler P.J., Blandin G., Berriman M., Crabtree J.,
RA   Aggarwal G., Caler E., Renauld H., Worthey E.A., Hertz-Fowler C.,
RA   Ghedin E., Peacock C., Bartholomeu D.C., Haas B.J., Tran A.-N.,
RA   Wortman J.R., Alsmark U.C.M., Angiuoli S., Anupama A., Badger J.,
RA   Bringaud F., Cadag E., Carlton J.M., Cerqueira G.C., Creasy T.,
RA   Delcher A.L., Djikeng A., Embley T.M., Hauser C., Ivens A.C.,
RA   Kummerfeld S.K., Pereira-Leal J.B., Nilsson D., Peterson J.,
RA   Salzberg S.L., Shallom J., Silva J.C., Sundaram J., Westenberger S.,
RA   White O., Melville S.E., Donelson J.E., Andersson B., Stuart K.D.,
RA   Hall N.;
RT   "Comparative Genomics of Trypanosomatid Parasitic Protozoa.";
RL   Science 0:0-0(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CL Brener;
RA   El-Sayed N., Bartholomeu D., Haas B.;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC   EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC   preliminary data.
CC   ---
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---
DR   EMBL; AAHK01008802; EAN88969.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   878 AA; 97344 MW; 6CA2E079914E4379 CRC64;

Qy   5 TLLLLLLLLKGSCLEWGLVGAQKVSSAATDAPIRDWAFFPPSFLCL------------- 52
         :|||||| ||||||||||||||||||||||||||||||||||||||
Db 796 TIVLVLLLSNGTC-------------VGLSLDGKVHDLGFLSPSFSSLPSCTLGTLTIEDLPH 845

Qy   53 RPAMTCSQAQPRG 65
         ||:||
Db 846 VSSLIMRHVKVNG 858

Best Local Similarity   18.4%;   Score 71;   DB 2;   Length 878;
Matches   20;   Conservative   9;   Mismatches   22;   Indels   22;   Gaps   2;

Query Match   27.4%;   Pred. No. 30;

RESULT 10
ID   CK5P3_HUMAN   STANDARD;   PRT;   506 AA.
AC   Q96JB5; Q53FA2; Q9H3F8; Q9H8GO; Q9HBR9;
DT   16-JUN-2003, integrated into UniProtKB/Swiss-Prot.
DT   16-JUN-2003, sequence version 2.
DT   07-MAR-2006, entry version 30.
DE   CDK5 regulatory subunit-associated protein 3 (CDK5 activator-binding
DE   protein C53) (HSF-27 protein).
GN   Name=CDK5RAP3; Synonyms=IC53; ORFNames=MSTP016, OK/SW-cl.114, P1553;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2), AND TISSUE SPECIFICITY.
RC   TISSUE=Aorta;
RX   MEDLINE=22050200; PubMed=12054757; DOI=10.1016/S0006-291X(02)00446-1;
RA   Chen J., Liu Y.Q., Han Y., Yu H., Zhang Y., Lu L., Zhen Y.,
RA   Hui R.T.;
RT   "A novel gene IC53 stimulates ECV304 cell proliferation and is
RT   upregulated in failing heart.";
RL   Biochem. Biophys. Res. Commun. 294:161-166(2002).
RN   [2]

RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 3), FUNCTION, AND TISSUE
RP   SPECIFICITY.
RC   TISSUE=Placenta;
RX   PubMed=12737517;
RA   Xie Y.H., He X.H., Tang Y.T., Li J.J., Pan Z.M., Qin W.X., Wan da F.,
RA   Gu J.R.;
RT   "Cloning and characterization of human ICS3-2, a novel CDK5 activator
RT   binding protein.";
RL   Cell Res. 13:83-91(2003).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RC   TISSUE=Kidney;
RA   Favier A.-L., Harsi C., Chrobozcek J.;
RT   "Protein interacting with the receptor binding domain of enteric
RT   adenovirus serotype 41 fiber protein.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   TISSUE=Colon adenocarcinoma;
RA   Shichijo S., Itoh K.;
RT   "Identification of immuno-peptidmics that are recognized by tumor-
RT   reactive CTL generated from TIL of colon cancer patients.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   TISSUE=Placenta;
RX   PubMed=14702039; DOI=10.1038/ng1285;
RA   Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA   Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA   Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA   Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA   Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA   Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA   Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA   Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA   Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA   Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA   Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA   Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA   Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA   Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA   Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA   Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA   Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA   Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA   Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
RN   [6]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   TISSUE=Synovial cell;
RA   Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   TISSUE=Brain;
RX   MEDLINE=22382257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   TISSUE SPECIFICITY.
RX   MEDLINE=20184747; PubMed=10721722; DOI=10.1016/S0378-1119(99)00499-0;
RA   Ching Y.-P., Qi Z., Wang J.H.;
RT   "Cloning of three novel neuronal Cdk5 activator binding proteins.";
RL   Gene 242:285-294(2000).
CC   -!- FUNCTION: Potential regulator of CDK5 activity. May be involved in
CC   cell proliferation. Regulates CDK5 activity via its interaction
CC   with CDK5R1 (By similarity).
CC   -!- SUBUNIT: Interacts with CDK5R1. This interaction is prevented by
CC   the association between CDK5R1 and CDK5RAP3 (By similarity).
CC   Interacts with the enteric adenovirus serotype 41 fiber protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=3;
CC   Name=1;
CC   IsoId=Q96JB5-1; Sequence=Displayed;
CC   Name=2; Synonyms=ICS5;
CC   IsoId=Q96JB5-2; Sequence=VSP_007566, VSP_007567;
CC   Note=Due to an intron retention;
CC   Name=3; Synonyms=ICS3-2;
CC   IsoId=Q96JB5-3; Sequence=VSP_007568;
CC   Note=Due to intron retention. No experimental confirmation
CC   available;
CC   -!- TISSUE SPECIFICITY: Ubiquitous. Expressed in heart, brain,
CC   placenta, lung, liver, skeletal muscle, kidney and pancreas.
CC   Isoform 3 is expressed in kidney, liver, skeletal muscle and
CC   placenta.
CC   -!- PTM: Phosphorylated in vitro by CDK5 (By similarity).
CC   -!- SIMILARITY: Belongs to the CDK5RAP3 family.
CC   -!- CAUTION: Ref.3 sequence differs from that shown due to a
CC   frameshift in position 410.

DR   EMBL; AF110322; AAG39277.1; -; mRNA.
DR   EMBL; AF217982; AAG17225.1; -; mRNA.
DR   EMBL; AF343090; AAK69655.1; ALT_FRAME; mRNA.
DR   EMBL; AB062433; BAB93496.1; -; mRNA.
DR   EMBL; AK023722; BAB14657.1; -; mRNA.
DR   EMBL; AK223387; BAD97107.1; -; mRNA.
DR   EMBL; BC009957; AAH09957.1; -; mRNA.
DR   EMBL; BC072435; AAH72435.1; -; mRNA.
DR   Ensembl; ENSG00000108465; Homo sapiens.
DR   HGNC; HGNC:18673; CDK5RAP3.
DR   MIM; 608202; gene.
DR   LinkHub; Q96JB5;
DR   GO; GO:0042808; F:neuronal Cdc2-like kinase binding; NAS.
DR   GO; GO:0007420; P:brain development; NAS.
DR   GO; GO:0008283; P:cell proliferation; ISS.
DR   GO; GO:0000079; P:regulation of cyclin dependent protein kina...; ISS.
DR   GO; GO:0045664; P:regulation of neuron differentiation; NAS.
DR   InterPro; IPR008491; DUF773.
DR   InterPro; IPR013224; Sigma_r3_r4.
DR   PANTHER; PTHR14894; DUF773; 1.
DR   Pfam; PF05600; DUF773; 1.
KW   Alternative splicing; Phosphorylation.
FT   CHAIN   1   506   CDK5 regulatory subunit-associated
FT   protein 3.

```
FT   VARSPLIC      1    225                                  /FTId=PRO_000020516.
FT                                                           Missing (in isoform 3).
FT                                                           /FTId=VSP_007568.
FT   VARSPLIC      1     87                                  Missing (in isoform 2).
FT                                                           /FTId=VSP_007566.
FT   VARSPLIC     88    111       RYSSQRMKDWQEIIALYEKDNTYL -> MCVHPGACLPHVG
FT                                 VSWAEFPGHFS (in isoform 2).
FT                                 /FTId=VSP_007567.
FT   CONFLICT    113    113       E -> V (in Ref. 6).
FT   CONFLICT    406    406       E -> K (in Ref. 3).
FT   CONFLICT    443    443       Q -> E (in Ref. 6).
SQ   SEQUENCE    506 AA;   56921 MW;  A21E59A79E1F87E0 CRC64;

Qy      18  LEWGLVGAQKVSSATDAPIR-----DWAFFPPSFLCLLPHRPAMTCSQAQPRGEGEKVG  71
            ||:||     ||::|                :||   ::|||   ::|      |  |:
Db     267  IDWGDFGVEAVSEGTDSGISAEAAGIDWGIFPES-----DSKDPGGDGIDWG        313

Qy      72  D  72
            :
Db     314  D 314
```

Query Match 18.3%; Score 70.5; DB 1; Length 506;
Best Local Similarity 29.5%; Pred. No. 20;
Matches 18; Conservative 5; Mismatches 19; Indels 19; Gaps 2;

RESULT 11

CK5P3 PONPY
```
ID   CK5P3_PONPY    STANDARD;      PRT;   506 AA.
AC   Q5REX6;
DT   21-JUN-2005, integrated into UniProtKB/Swiss-Prot.
DT   21-DEC-2004, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   CDK5 regulatory subunit-associated protein 3.
GN   Name=CDK5RAP3;
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Kidney;
RG   The German cDNA consortium;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Potential regulator of CDK5 activity. May be involved in
CC       cell proliferation. Regulates CDK5 activity via its interaction
CC       with CDK5R1 (By similarity).
CC   -!- SUBUNIT: Interacts with CDK5R1. This interaction is prevented by
CC       the association between CDK5R1 and CDK5RAP3 (By similarity).
CC   -!- PTM: Phosphorylated in vitro by CDK5 (By similarity).
CC   -!- SIMILARITY: Belongs to the CDK5RAP3 family.
CC   -----------------------------------------------------------------------
```
```
DR   EMBL; CR857387; CAH89681.1; -; mRNA.
DR   InterPro; IPR008491; DUF773.
DR   PANTHER; PTHR14894; DUF773; 1.
DR   Pfam; PF05600; DUF773; 1.
KW   Phosphorylation.
FT   CHAIN         1    506       CDK5 regulatory subunit-associated
FT                                protein 3.
FT                                /FTId=PRO_000220518.
SQ   SEQUENCE    506 AA;   56946 MW;  E756A359FE5437D6 CRC64;

Qy      18  LEWGLVGAQKVSSAIDAPIR-----DWAFFPPSFLCLLPHRPAMTCSQAQPRGEGEKVG  71
            ||:||     ||::|                :||   ::|||   ::|      |  |:
Db     267  IDWGDFGVEAVSEGTDSGISAKAAGIDWGIFPES-----DSKDPGGDGIDWG        313
```

Query Match 18.3%; Score 70.5; DB 1; Length 506;
Best Local Similarity 29.5%; Pred. No. 20;
Matches 18; Conservative 5; Mismatches 19; Indels 19; Gaps 2;

RESULT 12

DCH_THAAR
```
ID   DCH_THAAR      STANDARD;      PRT;   257 AA.
AC   087873;
DT   24-OCT-2001, integrated into UniProtKB/Swiss-Prot.
DT   24-OCT-2001, sequence version 2.
DT   07-FEB-2006, entry version 27.
DE   Cyclohexa-1,5-dienecarbonyl-CoA hydratase (EC 4.2.1.100) (Cyclohexa-
DE   1,5-diene-1-carboxyl-CoA hydratase) (Dienoyl-CoA hydratase).
GN   Name=dch;
OS   Thauera aromatica.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales;
OC   Rhodocyclaceae; Thauera.
OX   NCBI_TaxID=59405;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=98417440; PubMed=9746358;
RA   Breese K., Boll M., Alt-Moerbe J., Schaegger H., Fuchs G.;
RT   "Genes coding for the benzoyl-CoA pathway of anaerobic aromatic
RT   metabolism in the bacterium Thauera aromatica.";
RL   Eur. J. Biochem. 256:148-154(1998).
RN   [2]
RP   PROTEIN SEQUENCE OF 1-20, AND CHARACTERIZATION.
RX   MEDLINE=98409281; PubMed=9738901;
RA   Laempe D., Eisenreich W., Bacher A., Fuchs G.;
RT   "Cyclohexa-1,5-diene-1-carbonyl-CoA hydratase, an enzyme involved in
RT   anaerobic metabolism of benzoyl-CoA in the denitrifying bacterium
RT   Thauera aromatica.";
RL   Eur. J. Biochem. 255:618-627(1998).
CC   -!- FUNCTION: Catalyzes the hydration of cyclohexa-1,5-diene-1-
CC       carboxyl-CoA.
CC   -!- CATALYTIC ACTIVITY: Cyclohexa-1,5-dienecarbonyl-CoA + H(2)O = 6-
CC       hydroxycyclohex-1-enecarbonyl-CoA.
CC   -!- PATHWAY: Aromatic compounds metabolism via benzoyl-CoA.
CC   -!- SIMILARITY: Belongs to the enoyl-CoA hydratase/isomerase family.
CC   -----------------------------------------------------------------------
```
```
DR   EMBL; AJ224959; CAA12246.1; -; Genomic_DNA.
DR   InterPro; IPR001753; EnCoA_hydratase.
DR   Pfam; PF00378; ECH; 1.
DR   PROSITE; PS00166; ENOYL_COA_HYDRATASE; FALSE_NEG.
KW   Aromatic hydrocarbons catabolism; Direct protein sequencing; Lyase.
FT   INIT_MET      0      0
FT   CHAIN         1    257       Cyclohexa-1,5-dienecarbonyl-CoA
FT                                hydratase.
FT                                /FTId=PRO_000109323.
SQ   SEQUENCE    257 AA;   27751 MW;  50F4E61A868BF2C CRC64;

Qy       9  LLLLLLKGSCLEWGL---VGAQKVSSATDA-----PIRDWAFFPPSFLCLLPHRPAMTCSQ-  60
            ::|:||  ::|| ||      ||::|         |::  :|||   ::|||:  :|
Db      98  ILVALRGCLGGGLEVAAAGNILFAAPDAKFGQPEIRLGVFAPAASCLLPPRVGQACAED     157

Qy      61  AQPRGEGEKVG  71
               :      :
Db     158  LLWSGRSIDGAEGHRIG                                                174
```

Query Match 18.1%; Score 70; DB 1; Length 257;
Best Local Similarity 28.6%; Pred. No. 12;
Matches 22; Conservative 11; Mismatches 30; Indels 14; Gaps 3;

RESULT 13

Q6IGC8 DROME
```
ID   Q6IGC8_DROME   PRELIMINARY;   PRT;   130 AA.
AC   Q6IGC8;
```

```
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 8.
GN   ORFNames=HDC06620.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=14709175; DOI=10.1186/gb-2003-5-1-r3;
RA   Hild M., Beckmann B., Haas S.A., Koch B., Solovyev V., Busold C.,
RA   Fellenberg K., Boutros M., Vingron M., Sauer F., Hoheisel J.D.,
RA   Paro R.;
RT   "An integrated gene annotation and transcriptional profiling approach
RT   towards the full gene content of the Drosophila genome.";
RL   Genome Biol. 5:RESEARCH0003.1-RESEARCH0003.17(2003).
CC   -!- MISCELLANEOUS: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ third party annotation (TPA) entry.
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; BK003838; DAA02536.1; -; Genomic_DNA.
SQ   SEQUENCE   130 AA;  14460 MW;  34195AF7682CAFD7 CRC64;
```

```
Query Match             18.0%;  Score 69.5;  DB 2;  Length 130;
Best Local Similarity   30.7%;  Pred: No. 7;
Matches   27;  Conservative   7;  Mismatches   19;  Indels   35;  Gaps   5;

Qy      4 LTILILILILLKGSCLEWGLVGAQKVSSATD------------API-RDW-AFPPP---------- 44
            :||||||||||::|| ||||||||||::||                |  ||| ||||
Db     12 MLILILLLLLLQRGCCRWSMMGCNNNNHAANSKNNFSMLATIGRFWTAPFPPPRRNMEVDPE 71

Qy     45 ----------SFCLCLLP-HRPAM 56
                       ||| ||| | ||:
Db     72 VDVDHLDLNSQLANGGMLMLLPGHVPAI 99
```

```
RESULT 14

ID   KREM2_HUMAN             STANDARD;      PRT;    462 AA.
AC   Q8NCW0; Q8N2U4; Q96GL8; Q96GL9; Q8BTP9;
DT   23-APR-2003, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 27.
DE   Kremen protein 2 precursor (Kringle-containing protein marking the eye
DE   and the nose) (Dickkopf receptor 2).
GN   Name=KREMEN2; Synonyms=KRM2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], AND ALTERNATIVE SPLICING.
RA   Tanaka S., Sugimachi K.;
RT   "Human Kremen2 and Wnt signaling.";
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 3 AND 4).
RC   TISSUE=Ovarian carcinoma;
RX   PubMed=14702039; DOI=10.1038/ng1285;
RA   Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA   Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA   Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA   Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA   Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA   Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA   Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA   Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA   Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA   Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA   Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA   Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA   Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA   Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA   Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA   Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA   Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA   Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA   Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 3 AND 4).
RC   TISSUE=Brain, and Uterus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf
CC       to block Wnt/beta-catenin signaling. Forms a ternary complex with
CC       Dkk1 and LRP6 and induces rapid endocytosis and removal of the Wnt
CC       receptor LRP6 from the plasma membrane (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC       protein (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=1;
CC         IsoId=Q8NCW0-1; Sequence=Displayed;
CC       Name=2; Synonyms=Kremen2a;
CC         IsoId=Q8NCW0-2; Sequence=VSP_050509, VSP_050510;
CC       Name=3; Synonyms=Kremen2b;
CC         IsoId=Q8NCW0-3; Sequence=VSP_050511, VSP_050512;
CC       Name=4; Synonyms=Kremen2c;
CC         IsoId=Q8NCW0-4; Sequence=VSP_050513, VSP_050514;
CC   -!- SIMILARITY: Contains 1 CUB domain.
CC   -!- SIMILARITY: Contains 1 kringle domain.
CC   -!- SIMILARITY: Contains 1 WSC domain.
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; AB086405; BAC00872.1; -; mRNA.
DR   EMBL; AB086355; BAC00823.1; -; mRNA.
DR   EMBL; AB086356; BAC00824.1; -; mRNA.
```

Left column

```
DR   EMBL; AB086357; BAC00825.1; -; mRNA.
DR   EMBL; AK027669; BAB55281.1; -; mRNA.
DR   EMBL; AK075033; BAC11365.1; -; mRNA.
DR   EMBL; BC003533; AAH03533.1; -; mRNA.
DR   EMBL; BC009383; AAH09383.1; -; mRNA.
DR   HSSP; P00750; 1PK2.
DR   Ensembl; ENSG00000131650; Homo sapiens.
     HGNC; HGNC:18797; KREMEN2.
DR   InterPro; IPR000859; CUB.
DR   InterPro; IPR000859; CUB.
DR   InterPro; IPR002889; WSC_carb_bd.
DR   Pfam; PF00431; CUB; 1.
DR   Pfam; PF00051; Kringle; 1.
DR   Pfam; PF01822; WSC; 1.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000995; Kringle; 1.
DR   SMART; SM00042; CUB; 1.
DR   SMART; SM00130; KR; 1.
DR   PROSITE; PS01180; CUB; 1.
DR   PROSITE; PS00021; KRINGLE_1; 1.
DR   PROSITE; PS50070; KRINGLE_2; 1.
KW   Alternative splicing; Glycoprotein; Kringle; Membrane; Signal;
KW   Transmembrane; Wnt signaling pathway.
FT   SIGNAL        1     25       Potential.
FT   CHAIN        26    462       Kremen protein 2.
FT                                /FTId=PRO_0000021568.
FT   TOPO_DOM     26    364       Extracellular (Potential).
FT   TRANSMEM    365    387       Potential.
FT   TOPO_DOM    388    462       Cytoplasmic (Potential).
FT   DOMAIN       35    119       Kringle.
FT   DOMAIN      121    215       WSC.
FT   DOMAIN      219    326       CUB.
FT   CARBOHYD     49     49       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    222    222       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    244    244       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    351    351       N-linked (GlcNAc...) (Potential).
FT   DISULFID     36    119       By similarity.
FT   DISULFID     60    100       By similarity.
FT   DISULFID     89    114       By similarity.
FT   DISULFID    219    245       By similarity.
FT   VARSPLIC    367    420       ARVFSTVTAVSVLLLLLGLLRPLRRRSCLLAPGKGPPALG
FT                                ASRGPRRSWAVWY -> GAVCWLREKGPRRWGLPGAPGEAG
FT                                LCGTNSPEGWPCPAPGTPRLRVLPRATGL (in
FT                                isoform 3)
FT                                /FTId=VSP_050511.
FT   VARSPLIC    367    399       ARVFSTVTAVSVLLLLLGLLRPLRRRSCLLAP -> GEAG
FT                                ARDGSESGSRPLAPILTAAVCPQPGSSR (in isoform
FT                                4).
FT                                /FTId=VSP_050513.
FT   VARSPLIC    394    424       SCLLAPGKGFPALGASRGPRRSWAVWYQQPR -> CGALGQ
FT                                GLRADRWGAGAPEGNRARKELLGS (in isoform 2).
FT                                /FTId=VSP_050509.
FT   VARSPLIC    400    462       Missing (in isoform 4).
FT                                /FTId=VSP_050514.
FT   VARSPLIC    421    462       Missing (in isoform 3).
FT                                /FTId=VSP_050512.
FT   VARSPLIC    425    462       Missing (in isoform 2).
FT                                /FTId=VSP_050510.
FT   CONFLICT    164    202       Missing (in Ref. 2; BAC11365).
FT   CONFLICT    285    285       A -> D (in Ref. 2; BAC11365).
SQ   SEQUENCE   462 AA;  48849 MW;  CE3301591?A9A68 CRC64;

Qy  Query Match             17.9%;  Score 69;  DB 1;  Length 462;
    Best Local Similarity   33.8%;  Pred. No. 27;
    Matches   24;  Conservative    7;  Mismatches   34;  Indels    6;  Gaps    2;

Qy          1 MLLLLLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFPPPSFLCLLLPHRPAMTCSQ 60
              |||||||||||||||||||||||||
Db        379 LLLLLGLLRPLRRRSCLLAPGKGPPAL-GASRGPRRSWAVWYQQ----PRGVALPCSP 432

Qy         61 AQPRGEGEKVG 71
              |||||||||
Db        433 GDPQAEGSAAG 443
```

Right column

```
RESULT 15
Q4RTS7_TETNG
ID   Q4RTS7_TETNG            PRELIMINARY;   PRT;   652 AA.
AC   Q4RTS7;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Chromosome 2 SCAF14997, whole genome shotgun sequence. (Fragment).
GN   ORFNames=GSTENG00029115001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetraodontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15496914; DOI=10.1038/nature03025;
RA   Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   -!- SIMILARITY: Belongs to the ABC transporter family.
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; CAAE01014997; CAG08205.1; -; Genomic_DNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0016887; F:ATPase activity; IEA.
DR   GO; GO:0042626; F:ATPase activity, coupled to transmembrane m...; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR011527; ABC_TM_1.
DR   InterPro; IPR003439; ABC_transp_like.
DR   Pfam; PF00664; ABC_membrane; 1.
DR   Pfam; PF00005; ABC_tran; 1.
DR   SMART; SM00382; AAA; 1.
DR   ProDom; PD000006; ABC_transporter; 1.
DR   PROSITE; PS50929; ABC_TMF; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW   ATP-binding; Nucleotide-binding.
FT   NON_TER       1      1
FT   NON_TER     652    652
SQ   SEQUENCE   652 AA;  72132 MW;  515BDEFCDFF1515 CRC64;

Qy  Query Match             17.9%;  Score 69;  DB 2;  Length 652;
    Best Local Similarity   56.7%;  Pred. No. 38;
    Matches   17;  Conservative    0;  Mismatches   38;  Indels    6;  Gaps    2;
```

```
Qy     44  PSFLCLLPHRPAMTCSQAQPRGEGEKVGDG  73
           || |||||||| | |||
Db    450  PSLLCLLPH-VAATCS-----GESEPAGPG  473
```

Search completed: June   6, 2006, 21:38:37
Job time : 297 secs

OM protein - protein search, using sw model

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration ltd.

Run on: June 6, 2006, 21:33:55 ; Search time 39 Seconds
                                            (without alignments)
                                            180.098 Million cell updates/sec

Title: US-10-063-534-30
Perfect score: 386
Sequence: 1 MLLILTLLLLILLKGSCLEW..........PAMTCSQAQPRGEGEKVGDG 73

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	70.5	18.3	419	2	JC7863	IC53 protein - hum
2	67.5	17.5	669	2	A49585	Na+ channel protei
3	65.5	17.0	3788	2	T13960	beige protein homo
4	63.5	16.5	277	2	I52825	gene MAC25 protein
5	63.5	16.5	278	2	T46458	hypothetical prote
6	63.5	16.5	282	2	S50031	prostacyclin-stimu
7	63	16.3	141	1	HARNW	hypothetical 82K p
8	63	16.3	141	1	A25477	hemoglobin alpha c
9	62.5	16.2	270	2	S56160	hemoglobin alpha c
10	62.5	16.2	283	2	B83618	mast cell tryptase
11	62	16.1	141	2	A23571	probable CoA trans
12	62	16.1	496	2	O4BOC2	hemoglobin alpha c
13	62	16.1	1240	2	DJBE21	steroid 21-monooxy
14	61.5	15.9	148	2	AB3004	DNA-directed DNA p
15	61.5	15.9	148	2	G98279	hypothetical prote
16	61.5	15.9	326	2	AB3100	hypothetical prote
17	61.5	15.9	326	2	H98186	probable mikimopin
18	61.5	15.9	365	2	JH0534	class I histocompa
19	61	15.8	784	2	JQ0317	hypothetical prote
20	60.5	15.7	273	1	HLHUAW	MHC class I histoc
21	60.5	15.7	273	1	HLHU69	MHC class I histoc
22	60.5	15.7	274	1	HLHU32	MHC class I histoc
23	60.5	15.7	275	1	HLHU10	MHC class I histoc
24	60.5	15.7	357	2	S18198	class I histocompa
25	60.5	15.7	365	1	HLHUA2	MHC class I histoc
26	60.5	15.7	365	2	I38443	gene HLA-A-0203 pr
27	60.5	15.7	365	2	A45847	MHC class I histoc
28	60.5	15.7	365	2	I61902	MHC class I histoc
29	60.5	15.7	365	2	I38441	gene HLA-A-6802 pr
30	60.5	15.7	365	2	I37470	HLA-A*0210 - human
31	60.5	15.7	365	2	I84448	MHC class I histoc
32	60.5	15.7	365	2	JH0536	class I histocompa
33	60.5	15.7	365	2	I37477	MHC class I histoc
34	60.5	15.7	365	2	I37483	HLA-Aw34.2 antigen
35	60.5	15.7	365	2	I37482	MHC class I histoc
36	60.5	15.7	365	2	I61857	MHC HLA-A2.4a chai
37	60.5	15.7	365	2	I38442	gene HLA-A-0205 pr
38	60	15.5	142	1	HAMS	hemoglobin alpha c
39	60	15.5	492	1	A2252S	steroid 21-monooxy
40	59.5	15.4	317	2	I46916	insulin-like growt
41	59.5	15.4	365	2	I37542	MHC class I histoc
42	59.5	15.4	365	2	JH0535	class I histocompa
43	59.5	15.4	365	2	JT0135	MHC class I histoc
44	59.5	15.4	446	2	A34794	B-cell CLL/lymphom
45	59.5	15.4	1805	2	A34736	nestin - rat

ALIGNMENTS

RESULT 1
JC7863
IC53 protein - human
C;Species: Homo sapiens (man)
C;Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 21-Apr-2003
C;Accession: JC7863
R;Chen, J.; Liu, B.; Liu, Y.; Han, Y.; Yu, H.; Zhang, Y.; Lu, L.; Zhen, Y.; Hui, R.
Biochem. Biophys. Res. Commun. 294, 161-166, 2002
A;Title: A novel gene IC53 stimulates ECV304 cell proliferation and is upregulated in fa
A;Reference number: JC7863; MUID:22050200; PMID:12054757
A;Accession: JC7863
A;Molecule type: mRNA
A;Residues: 1-419 <CHE>
C;Cross-references: UNIPARC:UPI00000723B0; GB:AF110322
C;Comment: This protein, a homolog of C53 protein, is an intracellular protein. It is a
formation in blood-deprived heart tissues.
C;Genetics:
A;Gene: ic53
A;Map position: 17q21.31
C;Keywords: cardiac muscle; heart

Query Match	18.3%;	Score 70.5;	DB 2;	Length 419;
Best Local Similarity	29.5%;	Pred. No. 1.7;		
Matches	18;	Conservative	5;	Mismatches	19;	Indels	19;	Gaps	2;

Qy 18 LEWGLIVGAQKVSSATDAPIR-------DWAFPPPSFLCLLPHRPAMTCSQAQPRGEGEKVG 71
        :||| : || | || | ::| || | |
Db 180 IDWGDFGVEAVSEGTDSGISAEBAAGIDWGIFPES---------------DSKDPGDGIDWG 226

Qy 72 D 72
        D
Db 227 D 227

RESULT 2
A49585
Na+ channel protein, amiloride-sensitive - human
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
C;Accession: A49585; I51911
R;Voilley, N.; Lingueglia, E.; Champigny, G.; Mattei, M.G.; Waldmann, R.; Lazdunski, M.;
Proc. Natl. Acad. Sci. U.S.A. 91, 247-251, 1994
A;Title: The lung amiloride-sensitive Na+ channel: biophysical properties, pharmacology,
A;Reference number: A49585; MUID:94105144; PMID:8278374
A;Accession: A49585
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-669 <RES>
A;Cross-references: UNIPROT:P37088; UNIPARC:UPI00000000DC4; EMBL:X76180; NID:g4526649; PID
R;McDonald, F.J.; Snyder, P.M.; McCray, P.B.
Am. J. Physiol. 266, L728-L734, 1994
A;Title: Cloning, expression, and tissue distribution of a human amiloride-sensitive Na+

A;Reference number: I51911; MUID:9425729; PMID:8023962
A;Accession: I51911
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-669 <RE2>
A;Cross-references: UNIPARC:UPI0000000DC4; GB:L29007; NID:g493125; PIDN:AAA21813.1; PID:
A;Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I repe
A;Map position: 12p13
C;Genetics:

```
Query Match             17.5%;  Score 67.5; DB 2; Length 669;
Best Local Similarity   33.8%;  Pred. No. 5.9;
Matches 22;  Conservative 9;  Mismatches 21;  Indels 13;  Gaps 3;

Qy    3 LTLLLLLLLLKGSCLEW-----GLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTC 58
          ||||| ||  ||
Db  576 LIVIMFLMLLRRFRSRYWSPGRGGRGAQEVASTL------ASSPPSHFC--PHPMSLSL 626

Qy   59 SQAQP 63
          ||
Db  627 SQPGP 631
```

RESULT 3
T13960
beige protein homolog - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13960
R;Mori, M.; Nishikawa, T.; Higuchi, K.; Nishimura, M.
submitted to the EMBL Data Library, November 1998
A;Description: Deletion in the beige rat due to recombination between
A;Reference number: Z17837
A;Accession: T13960
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3788 <MOR>
A;Cross-references: UNIPROT:Q9Z2X9; UNIPARC:UPI00000E587B; EMBL:AB020019; NID:d1241953;
A;Experimental source: strain DA; spleen
C;Genetics:
A;Gene: beige

```
Query Match             17.0%;  Score 65.5; DB 2; Length 3788;
Best Local Similarity   33.3%;  Pred. No. 52;
Matches 22;  Conservative 9;  Mismatches 25;  Indels 9;  Gaps 3;

Qy    4 LTLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLL-LPHRPAMT--CSQ 60
          |||||||||
Db 1349 LTLLLRIFLEKSPCTEILLLHGIQKIVES------DFTMSFSQYLFPPLLHTPSLSNGVSS 1402

Qy   61 AQPRG 65
          ||
Db 1403 QKPPG 1407
```

RESULT 4
I52825
gene MAC25 protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Dec-2004
C;Accession: I52825
A;Reference number: I52825; MUID:94059820; PMID:7694637
A;Title: Identification and characterization of genes differentially expressed in mening
R;Murphy, M.; Pykett, M.J.; Harnish, P.; Zang, K.D.; George, D.L.
Cell Growth Differ. 4, 715-722, 1993
A;Accession: I52825
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-277 <RES>
A;Cross-references: UNIPROT:Q16270; UNIPARC:UPI000016ACFE; GB:L19182; NID:g307150; PIDN:
A;Genetics:
A;Gene: MAC25
C;Superfamily: IGFBP-related protein, MAC25 type; Kazal proteinase inhibitor homology

F;104-156/Domain: Kazal proteinase inhibitor homology <KPI8>

```
Query Match             16.5%;  Score 63.5; DB 2; Length 277;
Best Local Similarity   38.8%;  Pred. No. 7.5;
Matches 27;  Conservative 1;  Mismatches 29;  Indels 13;  Gaps 3;

Qy    6 LTLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFP-PSFLCLLPH-RPAMTCSQAQP 63
          |||||||||
Db   16 LTLLLLPLSSSS-----------SSDTCGPCEPASCPPLPLGCLLGETRDACGGCCPMCA 64

Qy   64 RGEGEKVGDG 73
          ||||
Db   65 RGEGEPCGGG 74
```

RESULT 5
T46458
hypothetical protein DKFZp434M102.1 - human (fragment)
C;Species: Homo sapiens (man)
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-278 <AAA>
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46458
R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23028
A;Accession: T46458
A;Cross-references: UNIPROT:Q9NTB5; UNIPARC:UPI0000007047B; EMBL:AL137404
A;Experimental source: adult testis; clone DKFZp434M102
C;Genetics:
A;Note: DKFZp434M102.1

```
Query Match             16.5%;  Score 63.5; DB 2; Length 278;
Best Local Similarity   24.2%;  Pred. No. 7.5;
Matches 24;  Conservative 11;  Mismatches 29;  Indels 35;  Gaps 4;

Qy    2 LLLTLLLLLLLL------------KGSCLEWGLV-------------------GAQKVSSA 31
          |||||||||
Db   84 MALTFLLVLILTLATLCTRLHRNFRRGESIYWGPTADSQDTVAGEEFPPYPTRGPRPFSRR 143

Qy   32 TDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQPRGEGEKV 70
          |||||
Db  144 PAAP-RSFPALPP----LTARRPAHSCAEAEAAAASRRV 177
```

RESULT 6
S50031
prostacyclin-stimulating factor - human
A;Title: Purification and molecular cloning of prostacyclin-stimulating factor from serum
R;Yamauchi, T.; Umeda, F.; Masakado, M.; Isaji, M.; Mizushima, S.; Nawata, H.
Biochem. J. 303, 591-598, 1994
A;Accession: S50031
A;Status: preliminary
A;Reference number: S50031; MUID:95071263; PMID:7980422
C;Species: Homo sapiens (man)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 31-Dec-2004
C;Accession: S50031
A;Residues: 1-282 <YAM>
A;Molecule type: mRNA
A;Cross-references: UNIPROT:Q16270; UNIPARC:UPI00000042D2; GB:S75725; NID:g861520; PIDN:
A;Superfamily: IGFBP-related protein, MAC25 type; Kazal proteinase inhibitor homology <KPI8>
F;104-156/Domain: Kazal proteinase inhibitor homology <KPI8>

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Query Match             16.5%;  Score 63.5; DB 2; Length 282;
Best Local Similarity   38.6%;  Pred. No. 7.6;
Matches 27;  Conservative 1;  Mismatches 29;  Indels 13;  Gaps 3;

Qy    6 LTLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFP-PSFLCLLPH-RPAMTCSQAQP 63
          |||||||||
Db   16 LTLLLLPLSSSS-----------SSDTCGPCEPASCPLPLGCLLGETRDACGCCPMCA 63

Qy   64 RGEGEKVGDG 73
          ||||
Db   64 RGEGEPCGGG 73
```

RESULT 7
Db HARNW

65 RGEGEPCGGG 74
||||| ||

hemoglobin alpha chain - white rhinoceros
C;Species: Ceratotherium simum (white rhinoceros, square-lipped rhinoceros)
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 12-Jul-2004
C;Accession: A02286
R;Mazur, G.; Braunitzer, G.; Wright, P.G.
Hoppe-Seyler's Z. Physiol. Chem. 363, 1077-1085, 1982
A;Title: Die Primaerstruktur des Haemoglobins vom Breitmaulnashorn (Ceratotherium simum,
A;Reference number: A91701; MUID:83055102; PMID:7141412
A;Accession: A02286
A;Molecule type: protein
A;Residues: 1-141 <MAZ>
A;Cross-references: UNIPROT:P01963; UNIPARC:UPI000012C15E
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrie
F;2-141/Domain: globin homology <GLB>
F;58/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match   16.3%; Score 63; DB 1; Length 141;
Best Local Similarity   35.8%;   Pred. No. 4.6;
Matches 19; Conservative 7; Mismatches 25; Indels 2; Gaps 2;

Qy   20 WGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSOAQPRGEGEKVGD 72
          || ||| ||| || ||:|||||||
Db   14 WGHVGAQAGEYGARALERMFLSFPTT-KTYPFHFD-LSHGSAQVKAHGKKVGD 64

RESULT 8
A25477
hemoglobin alpha chain - white-faced sapajou
C;Species: Cebus capucinus (white-faced sapajou, white-throated capuchin)
C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 12-Jul-2004
C;Accession: A25477
R;Tanioka, Y.; Araya, A.; Maita, T.; Matsuda, G.
Biol. Chem. Hoppe-Seyler 367, 147-152, 1986
A;Title: Primary structure of adult hemoglobin of white-throated capuchin, Cebus capucin
A;Reference number: A90702; MUID:86187258; PMID:3964444
A;Accession: A25477
A;Molecule type: protein
A;Residues: 1-141 <TAN>
A;Cross-references: UNIPROT:P07421; UNIPARC:UPI000012C15C
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; heme; iron; metalloprotein; oxygen carrier
F;2-141/Domain: globin homology <GLB>
F;58/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match   16.3%; Score 63; DB 2; Length 141;
Best Local Similarity   35.8%;   Pred. No. 4.6;
Matches 19; Conservative 6; Mismatches 26; Indels 2; Gaps 2;

Qy   20 WGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSOAQPRGEGEKVGD 72
          || ||| ||| || ||:|||||||
Db   14 WGHVGAQAGEYGAEALERMFLSFPTT-KTYPFHFD-LSHGSAQVKAHGKKVGD 64

RESULT 9
S56160
mast cell tryptase precursor - Mongolian jird
C;Species: Meriones unguiculatus (Mongolian jird)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S56160
R;Murakumo, Y.; Ide, H.; Itoh, H.; Tomita, M.; Kobayashi, T.; Maruyama, H.; Horii, Y.; N
Biochem. J. 309, 921-926, 1995
A;Title: Cloning of the cDNA encoding mast cell tryptase of Mongolian gerbil, Meriones u
A;Reference number: S56160; MUID:9366971; PMID:7639711

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-270 <MUR>
A;Cross-references: UNIPROT:P50342; UNIPARC:UPI00001371D; EMBL:D31789; NID:g511122; PIDI
A;Superfamily: trypsin; trypsin homology
F;26-262/Domain: trypsin homology <TRY>

Query Match   16.2%; Score 62.5; DB 2; Length 270;
Best Local Similarity   40.0%;   Pred. No. 9.6;
Matches 16; Conservative 5; Mismatches 12; Indels 7; Gaps 2;

Qy   1 MLLITLILLLLLIKGS-CLEWGLVGAQKVSSATDAPIRDW 39
          || ||| ||:| :|:|:||| ||||||||
Db   4 LILIALPLFSLMHRSPLCQEWGIVGGQ-----EAPGNKW 37

RESULT 10
B83618
probable CoA transferase, subunit A PA0226 [imported] - Pseudomonas aeruginosa (strain PA
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: B83618
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83618
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-283 <STO>
A;Cross-references: UNIPROT:Q9I6R2; UNIPARC:UPI00000C4FA9; GB:AE004460; GB:AE004091; NID
A;Experimental source: strain PA01
C;Genetics:
C;Gene: PA0226

Query Match   16.2%; Score 62.5; DB 2; Length 283;
Best Local Similarity   29.3%;   Pred. No. 10;
Matches 17; Conservative 7; Mismatches 11; Indels 23; Gaps 3;

Qy   14 KGSCLEWGLVGAQK------------------VSSATDAPIR-----DWAFFPPSFLCLLP 51
          || ||:|||| ::: ::: | | :|
Db   171 KGNVLLWGILGVGKEAALAAKCIVTVEEIVDELDAPMNACVLPSWAL---SAVCLVP 225

RESULT 11
A23571
hemoglobin alpha chain - southeastern quoll
C;Species: Dasyurus viverrinus (southeastern quoll)
C;Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 12-Jul-2004
C;Accession: A23571
R;Wainwright, B.; Hope, R.
Proc. Natl. Acad. Sci. U.S.A. 82, 8105-8108, 1985
A;Title: Cloning and chromosomal location of the alpha- and beta-globin genes from a mars
A;Reference number: A94077; MUID:86068050; PMID:3865220
A;Accession: A23571
A;Molecule type: mRNA
A;Residues: 1-141 <WAI>
A;Note: Initiator Met not shown
A;Cross-references: UNIPROT:P07419; UNIPARC:UPI000012C17I; GB:M14567; NID:g163892; PIDN:l
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; heme; iron; metalloprotein; oxygen carrier
F;2-141/Domain: globin homology <GLB>
F;58/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match   16.1%; Score 62; DB 2; Length 141;
Best Local Similarity   34.0%;   Pred. No. 6;
Matches 18; Conservative 8; Mismatches 25; Indels 2; Gaps 2;

Qy   20 WGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSOAQPRGEGEKVGD 72
          || ||| ||| || ||: ||| ||| | |||

Db   14 WGKVGGHAGAYAAFALARTFLSFPTT-KTYPFHFD-LSPGSAQIQGHGKKVAD 64

RESULT 12

O4BOC2

steroid 21-monooxygenase (EC 1.14.99.10) cytochrome P450 (C21); steroid 21-hydroxylase

N;Alternate names: cytochrome P450 21A1 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-May-1986 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
A;Reference number: A27555; A00192; A24101; C28860; A21181
C;Accession: A27555
A;Molecule type: DNA
A;Residues: 1-496 <CHU>
A;Cross-references: UNIPROT:P00191; UNIPARC:UPI000016F7C38; GB:M12918; NID:gl62947; PIDN:AAA30487.1; PID:
R;Tsurumi, T.; Maeno, K.; Nishiyama, Y.
J. Biol. Chem. 261, 4106-4109, 1986
A;Title: Structural analysis of cloned cDNA for mRNA of microsomal cytochrome P-450(C21)
A;Accession: A00192
A;Molecule type: mRNA
A;Residues: 1-13, 'S', 15-400, 'Y', 402-496 <YOS>
A;Cross-references: UNIPARC:UPI0000167C38; GB:M12918; NID:gl62947; PIDN:AAA30487.1; PID:
R;Yoshioka, H.; Morohashi, K.; Sogawa, K.; Yamane, M.; Kominami, S.; Takemori, S.; Okada
J. Biochem. 94, 1711-1714, 1983
A;Title: Bovine steroid 21-hydroxylase: regulation of biosynthesis.
A;Accession: A24101
A;Molecule type: mRNA
A;Residues: 121-430, 'C', 432-496 <OGS>
A;Cross-references: UNIPARC:UPI0000171D8D
R;Ogishima, T.; Okada, Y.; Kominami, S.; Takemori, S.; Omura, T.
J. Biochem. 94, 1711-1714, 1983
A;Title: Partial amino acid sequences of two mitochondrial and two microsomal cytochrome
A;Reference number: A91972; MUID:8408829; PMID:6654880
A;Accession: C28860
A;Molecule type: protein
A;Residues: 1-12, 'K', 14-15, 248-250, 'S' <OGS>
A;Cross-references: UNIPARC:UPI0000171D8D
A;Experimental source: adrenal cortex microsomes
Proc. Natl. Acad. Sci. U.S.A. 81, 1986-1990, 1984
A;Title: Cloning and expression of cDNA encoding a bovine adrenal cytochrome P-450 speci
A;Reference number: A21181; MUID:84193940; PMID:6609358
A;Contents: annotation; sequence report
A;Note: this sequence differs substantially from that in reference A24101
A;Genetics:
A;Introns: 68/1; 98/1; 149/3; 181/3; 215/3; 244/3; 311/3; 371/2; 406/1
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metallo
F;287-449/Domain: cytochrome P450 homology <P45>
F;427/Binding site: heme iron (Cys) (axial ligand) #status predicted

Qy   1 MLLLTLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLL-PHRPAMTCS 59
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MVLAGLLLLTLLAGAHLLW--GRWKLRNLHLPPL------VPGFLHLLQPNLPHLLS 51

RESULT 13
DJBE21
DNA-directed DNA polymerase (EC 2.7.7.7) - human herpesvirus 2 (strain 186)

C;Species: human herpesvirus 2
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A27315
A;Title: Nucleotide sequence of the DNA polymerase gene of herpes simplex virus type 2 an
A;Reference number: A27315; MUID:8727385; PMID:303677
A;Accession: A27315
A;Molecule type: DNA
A;Residues: 1-1240 <TSU>
A;Cross-references: UNIPROT:P07918; UNIPARC:UPI0000129007; GB:M16321; NID:g3302291; PIDN:A
C;Superfamily: DNA polymerase
C;Keywords: DNA binding; DNA replication; nucleotidyltransferase

Qy   51 PHRPAMTCSQAQPRGEGEKVGDG 73
        |||||||| |||||| |||
Db 652 PKRPAV-----PRGEGERPGDG 668

RESULT 14
AB3004
hypothetical protein Atu3636 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AB3004
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, J.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClella
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB3004
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-148 <KUR>
A;Cross-references: UNIPROT:Q8U9T9; UNIPARC:UPI000000D2299; GB:AE008689; PIDN:AAL4448.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu3636
A;Map position: linear chromosome

Qy   10 LLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLC------LLPHRPAM------ 56
        ::|:|:||||||||||||||||||||||||:|||||||| |:||||||||
Db   1 MILVEGTKLEF--GDGRVSAA--SPWRRWPSMANAFLVDINKQPGVRPHRPALLSACLR 55

RESULT 15
G98279
hypothetical protein AGR_L_2383 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: G98279
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
A;Reference number: A97355; MUID:21608551; PMID:11743194
A;Accession: G98279
A;Status: preliminary

Qy   51 PHRPAMTCSQAQPRGEGEKVGDG 73
        |||||||| |||||| |||

Query Match   16.1%;   Score 62;   DB 1;   Length 496;
Best Local Similarity   37.9%;   Pred. No. 19;
Matches   25;   Conservative   6;   Mismatches   25;   Indels   10;   Gaps   3;

Query Match   16.1%;   Score 62;   DB 1;   Length 1240;
Best Local Similarity   56.5%;   Pred. No. 46;
Matches   13;   Conservative   2;   Mismatches   2;   Indels   6;   Gaps   1;

Query Match   15.9%;   Score 61.5;   DB 2;   Length 148;
Best Local Similarity   29.0%;   Pred. No. 7.1;
Matches   20;   Conservative   14;   Mismatches   14;   Indels   21;   Gaps   4;

A;Molecule type: DNA
A;Residues: 1-148 <KUR>
A;Cross-references: UNIPROT:Q8U9T9; UNIPARC:UPI00000D2299; GB:AE007870; PIDN:AAK89761.1;
C;Genetics:
A;Gene: AGR_L_2383
A;Map position: linear chromosome

Query Match   15.9%;   Score 61.5; DB 2; Length 148;
Best Local Similarity   29.0%;   Pred. No. 7.1;
Matches   20; Conservative 14; Mismatches 14; Indels 21; Gaps 4;

Qy   10 LLLLKGSCLEWGLVGAQKVSSAATDAPIRDWAFFPPSFLC------LLPHRPAM----- 56
         ::||:|: |||: | | | |: |||| : | : ||||||:
Db   1 MILVEGTKLEF---GDGRVSAA--SPWRRWPSMANAFLVDINKQPGVRPHRPALLSACLR 55

Qy   57 ---TCSQAQ 62
            :|| :
Db   56 TLHSCSDVE 64

Search completed: June 6, 2006, 21:39:20
Job time : 41 secs

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